us-09-294-298-5.rge

OM nucleic - nucleic search, using sw model

GenCore version 4.5
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Run on: January 18, 2001, 07:18:54 ; Search time 14302.9 Seconds
(without alignments)
1424.454 Million cell updates/sec

Title: US-09-294-298-5
Perfect score: 3981
Sequence: 1 tagggagagactgagctgcc..........tggggtgtgtatccccatcct 3981

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1118133 seqs, 2558875100 residues

Total number of hits satisfying chosen parameters: 2236266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :   GenEmbl:*

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 1: gb_bal:*        44: gb_pl3:*
 2: gb_ba2:*        45: gb_pr5:*
 3: gb_om:*         46: gb_htg8:*
 4: gb_ov:*         47: gb_htg9:*
 5: gb_ph:*         48: gb_htg10:*
 6: gb_pl1:*        49: gb_htg11:*
 7: gb_pl2:*        50: gb_htg12:*
 8: gb_pr1:*        51: gb_htg13:*
 9: gb_pr2:*        52: gb_htg14:*
10: gb_pr3:*        53: gb_in3:*
11: em_fun:*        54: gb_htg15:*
12: em_hum1:*       55: gb_htg16:*
13: em_hum2:*       56: gb_htg17:*
14: em_in:*         57: em_htg4:*
15: em_om:*         58: em_htg5:*
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17: em_ov:*         60: em_htg7:*
18: em_pat:*        61: em_hum6:*
19: em_ph:*         62: gb_htg18:*
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21: em_ro:*         64: gb_ba3:*
22: em_sts:*        65: em_htg8:*
23: em_sy:*         66: em_htg9:*
24: em_un:*         67: em_htg10:*
25: em_vi:*         68: gb_pr6:*
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29: gb_in2:*        72: gb_htg22:*
30: em_bal:*        73: gb_htg23:*
31: em_ba2:*        74: gb_ro:*
32: em_hum3:*       75: gb_sts1:*
33: em_hum4:*       76: gb_sts2:*
34: gb_pr4:*        77: gb_sy:*
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37: gb_htg5:*       80: gb_vi2:*
38: gb_htg6:*       81: gb_pat1:*
39: gb_htg7:*       82: gb_pat2:*
40: em_htg1:*       83: em_htg0:*
41: em_htg2:*       84: gb_htg24:*
42: em_htg3:*       85: gb_prt8:*
43: em_hum5:*
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SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3967	99.6	4265	74	AF050183	AF050183 Rattus no
2	3936.2	98.9	4140	74	AF058790	AF058790 Rattus no
3	3828.4	96.2	4539	74	AF058789	AF058789 Rattus no
4	3601.4	90.5	4063	74	AF048976	AF048976 Rattus no
5	3579.6	89.9	4801	74	AB016962	AB016962 Rattus no
6	920.8	23.1	94770	69	HSD570F3	AL050332 Human DNA
7	920.8	23.1	150956	70	AL161903	AL161903 Homo sapi
8	920.8	23.1	169323	70	AL161906	AL161906 Homo sapi
9	629.4	15.8	4368	10	AF047711	AF047711 Homo sapi
10	443.2	11.1	829	74	AF053938	AF053938 Rattus no
11	336.4	8.5	4287	34	AK024488	AK024488 Homo sapi
12	240.2	6.0	56366	39	AC019800	AC019800 Drosophil
13	240.2	6.0	191504	36	AC012162	AC012162 Drosophil
14	240.2	6.0	202741	36	AC012161	AC012161 Drosophil
15	240.2	6.0	300994	28	AE003506	AE003506 Drosophil
16	235.2	5.9	3984	28	AB011280	AB011280 Caenorhab
17	222	5.6	65961	38	AC016523	AC016523 Drosophil
18	206.8	5.2	2385	34	AK022662	AK022662 Homo sapi
19	196	4.9	172027	72	AL365274	AL365274 Homo sapi
20	194.4	4.9	211	74	AF055883	AF055883 Rattus no
21	187.6	4.7	169323	70	AL161906	AL161906 Homo sapi

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c 22   157   3.9  81971  HS593C16    AL035702 Human DNA
  23   157   3.9 156700  AC027051    AC027051 Homo sapi
  24   139.2 3.9 155332  AC027051    AC040900 Homo sapi
c 25   139.2 3.5 156700  AC040900    AC027051 Homo sapi
c 26   113.4 2.8   4107  MMU20238    U20238 Mus musculu
  27   113.4 2.8 159777  AC011703    AC011703 Drosophil
  28   103.4 2.6 157803  AC011492    AC011492 Homo sapi
  29    99.2 2.5   2837  HSINSP4BP   X89399 Homo sapien
  30    98.4 2.5  39660  CEC07B5     Z46266 Caenorhabdi
  31    98.4 2.5 237619  AC073765    AC073765 Mus muscu
  32    97.6 2.5    833  AB011285    AB011285 Caenorhab
  33    95.8 2.4   2647  E13125      E13125 Bovine gene
  34    95.8 2.4   2730  BTU30857    U30857 Bos taurus
  35    93.8 2.4    760  AB011283    AB011283 Caenorhab
  36    93.8 2.4   2276  AB011279    AB011279 Caenorhab
  37    89.2 2.2    314  G21290      G21290 human STS W
c 38    71.2 1.8    310  AB011284    AB011284 Caenorhab
  39    70.8 1.8   5719  MMCATS1     AF051726 Mus muscu
c 40    70.8 1.8 180385  AC007461    AC007461 Homo sapi
c 41    69.6 1.7   3720  S76368      S76368 ORF 5' of E
c 42    69.6 1.7  43658  HSV3PRGEN   M86409 Herpesvirus
c 43    69.6 1.7 112930  HSGEND      X64346 Herpesvirus
  44      68  1.7   5579  AB011110    AB011110 Homo sapi
c 45    67.4 1.7 314556  AC073495    AC073495 Mus muscu
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KEVFASWRLRCAERGREDIADRLISASLFLRFLCPAIMSPSLFGLMQEYPDEQTSRTL
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YIDLGRELSTLHALLWEVLPQLSKEALLKLGPLPRLLSDLSTALRNPNIORQPSROSE
RARSQPMVLRGPSAEMQGYMMRDLNSSIDLQSFMARGLNSSMDMARLPSPTKEKPPPP
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NSSSVSNLAAVGDLLHSSQASLTAALGLRPAPAGRLSQGSGSITAAGMRLSQMGVTT
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BASE COUNT    936 a   1358 c   1203 g    768 t
ORIGIN

Query Match          99.6%;  Score 3967;  DB 74;  Length 4265;
Best Local Similarity  99.9%;  Pred. No. 0;
Matches 3981;    Conservative 0;   Mismatches 0;   Indels 4;   Gaps 1:

Qy     1 taggagagactgagctgccccagcacccattccattgctcccagcaaggcttc   60
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Qy    61 ctgagccggagctaaaagctccatcaaagtacaaagtcacaaccaaacttgaccgg  120
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Db   154 CTGAGCCGGAGGCTAAAAGCTCCATCAAAGTACAAAGTCACAACCAAACTTGACCGG  213

Qy   121 accagcagctttcgacagatcctgccttccgaagtgctgaccatgacgggcccgg  180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   214 ACCAGCAGCTTTCGACAGATCCTGCCTTCCGAAGTGCTGACCATGACGGGCCCGG  273

Qy   181 ctgatgcagagcttcaaggagtctcactcccagtccctgctgagtcccagcagtgct  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   274 CTGATGCAGAGCTTCAAGGAGTCTCACTCCCAGTCCCTGCTGAGTCCCAGCAGTGCT  333

Qy   241 gctgaggccctggagctcaacctgatgaagactccattacaagccagtacaacagctcc  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   334 GCTGAGGCCCTGGAGCTCAACCTGATGAAGACTCCATTATCAAGCCAGTACAACAGCTCC  393

Qy   301 atcctgggccaggagttctgcttgaggtaacaacatcgtctgggacaaaatgttttggcc  360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   394 ATCCTGGGCCAGGAGTTCTGCTTTGAGGTAACAACATCGTCTGGGACAAAATGTTTTGCC  453

Qy   361 tgtcggtctgcagccgaaagggacaaatgattgagaatcacagagggctgtgaaaccc  420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   454 TGTCGGTCTGCAGCCGAAAGGGACAAATGATTGAGAATCACAGAGGGCTGTGAAACCC  513

Qy   421 aacaaggacaacagcacgccgggtagataacgtgctgaaactgctcataqaagctcga  480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   514 AACAAGGACAACAGCCACGCCGGGTAGATAACGTGCTGAAACTGCTCATAGAAGCTCGA  573

Qy   481 gagctgccccaagaagcgatattactgcgagttgtgccggacgacatgtctatgca  540
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Db   574 GAGCTGCCCCCAAGAAGCGATATTACTGCGAGTTGTGCCGGACGACATGTCTATGCA  633

Qy   541 cggaccacttccagccccgctcagcctcaggagacactgtctttgggcggagcacttc  600
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Db   634 CGGACCACTTCCAGCCCCGCTCAGCCTCAGGAGACACTGTCTTTTGGGGCGAGCACTTC  693

Qy   601 gagtttaacaacctgctcgtccggcgctgcgcatctgcatctgactcggac  660
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Db   694 GAGTTTAACAACCTGCTCTGCTCCGGCGCTGCCGCCTGTACCGTGACTCGGAC  753

Qy   661 aaaaagcggaagaaggacaggcaggctacgttgcctggtgactgttccagtggcacc  720
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Db   754 AAAAAGCGGAAGAAGGACAGGCAGGCTACGTTGCCTGGTGACTGTTCCAGTGGCACC  813

Qy   721 ctggctgggcgccaactcacagagcagtggtaccccgtgaccctgccaacaggaagtggg  780
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ALIGNMENTS

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RESULT    1
AF050183
LOCUS       AF050183    4265 bp    mRNA          ROD       15-SEP-2000
DEFINITION  Rattus norvegicus GTPase activating protein SynGAP-c mRNA, complete
            cds.
ACCESSION   AF050183
VERSION     AF050183.2   GI:10140854
KEYWORDS    .
SOURCE      Norway rat.
ORGANISM    Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 4265)
AUTHORS     Kim,J.H., Liao,D., Lau,L.F. and Huganir,R.L.
TITLE       SynGAP: a synaptic RasGAP that associates with the PSD-95/SAP90
            protein family
JOURNAL     Neuron 20 (4), 683-691 (1998)
MEDLINE     98240917
REFERENCE   2  (bases 1 to 4265)
AUTHORS     Kim,J.H. and Huganir,R.L.
TITLE       Direct Submission
JOURNAL     Submitted (20-FEB-1998) Neuroscience, Johns Hopkins Medical
            Institute, 725 N. Wolfe Street, PCTB 900, Baltimore, MD 21205, USA
COMMENT     On Sep 15, 2000 this sequence version replaced gi:3044054.
FEATURES             Location/Qualifiers
     source          1..4265
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                     /db_xref="taxon:10116"
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     CDS             277..3792
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                     PSD-95/SAP90 protein family; alternatively spliced
                     variants, SynGAP-a and SynGAP-b"
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                     /protein_id="AAC40082.2"
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                     /translation="MOSFKESHSHESLLSPSSAAEALENLDEDSIIKPVHSSILGQE
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                     PKKRYCELCLDDMLYARTTSKPRSASGDTVFWGEHEFEFNNLPAVRALRLHLYRDSDK
                     KRKDKAGYVGLVTVPVATLAGRHFTEQWYPVTLPTGSSGSGMGSGGGSGGGGSGG
                     KGKGGCPAVRLKARYQTMSILPMELYKEFAEYVTNHYRMLCAVLEPALNVKGKEEVAS
```

```
Db   1894  CCGCTGCCCCGGCTCCTCAGGCGACATCAGCAGCCCTGAGGAACCCTAACATCCAAAGG  1953
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1861  cagccgagccgccagacgacgcgctcggtctcagccacatggtgtcgcgggccgtca    1920
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1954  CAGCCGAGCCGCCAGACGCGAGCGCGTCGGTCTCAGCCCATGGTGTCGCGGGCCGTCA   2013

Qy   1921  gccgaaatgcagggctacatgatgcgggacctcaacagctcaacgactcagtccttc    1980
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Db   2014  GCCGAAATGCAGGGCTACATGATGCGGGACCTCAACAGCTCCATCGACCTTCAGTCCTTC  2073

Qy   1981  atggctcgaggctcaacagctctatgacatggctcgcctccctcccaaccaaggag     2040
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Db   2074  ATGGCTCGAGGCCTCAACAGCTTCATGGACATGGCTCGCCTCGCCTCCCAACCAAGGAG  2133

Qy   2041  aaaccccgcgccccctccggtggggtaaagacctgttctatgtgagcggccacca     2100
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2134  AAACCCCGCCGCCCCTCCCGGTGGGGTAAAGACCGTTCTATGTGAGCCGGCCACCA    2193

Qy   2101  ctggccggtcctcccagcatactgcacgagcagctcggaacatcacagagccggagcag  2160
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Db   2194  CTGGCCCGGTCCTCCCCAGCATACTGCACGAGCAGCTCGGACATCACAGAGCCGGAGCAG  2253

Qy   2161  aagatgctgagtgtcaacaagagtgtccatgtctggacctgcagggcacgggcctggg   2220
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Db   2254  AAGATGCTGAGTGTCAACAAGAGTGTGTCCATGTCTGGACCTGCCAGGGCCACGGGCCTGGG  2313

Qy   2221  ggccgccttaacagcagtagtgttccaacctggcagctgtgtgggacctgttgcactca  2280
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Qy   2281  agccaggcttcactgacgcagcctggggttgcggcctgcacctgccgggcgcctctcc   2340
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Qy   2341  caagggagtggctcttccatcacagcagccggatggtgccctcagccagatgggtgtcact  2400
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Db   2434  CAAGGGAGTGGCTCTTCCATCACAGCAGCAGCCCCCAGCAGCCCAGCATGGGTGTCACT   2493

Qy   2401  acggatggtgtccccgccagacaactcgcatccctcttccttcagaaccccctcttc   2460
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Qy   2461  catatgctgccgatggaccaggccccagacaggccatggaggggagcagtgccatggt  2520
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2554  CATATGCTGCCGATGGACCAGGCCCCAGCAGGCCCATGGAGGAGGAGCCAGTGGCCATGGT  2613

Qy   2521  ccacttcctcccatcacaccaccaccatcaccatcaccagggggagaaccccca      2580
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Qy   2581  ggggacacttttgccccgttccatggctatagcagagcgaggacctctctacggggtc   2640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2674  GGGGACAACTTTTGCCCCGTTCCCATGGCTATAGCAGCAAGAGCGAGGACCTCCTACAGGGGTC  2733

Qy   2641  cctaagcccctgcggcctcatccttcacagccacagtgatgagttggaccc      2700
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db   2734  CCTAAGCCCCCGCGGCCTCCCATCCTTCACAGCCACCAGCAGCTACAGTGGGTTTTGGACCCC  2793

Qy   2701  tcggtactgatttaccgtcggcagctcacttcaggacaacctcagcaacatgctc     2760
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2794  TCTGGTACTGATTTTACCCGTCGCCAGCTCTCACTTCAGGACAACCTACAGCACATGTCTC  2853

Qy   2761  tccccgcccagatcaccgtcggtcccagaggcagctccctcaggaggaggggc      2820
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Db   2854  TCCCCGCCCCAGATCACCATCCGGTCCCCAGAGGCCAGCTCCCTCAGGGGCCAGGAGGGGGC  2913

Qy   2821  agtggtggggcagtggtggggcggtggggccagccacctccttgcagaggggcaaa    2880
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Db   2914  AGTGGTGGGGCAGTGGTGGGGCGGTGGGGGCCAGCCACCTCCTTGCAGAGGGCAAA   2973

Qy   2881  tctcagcagttgacagtgagtgctgcccagaaacccgagctaacatccaaagg     2940
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Db   2974  TCTCAGCAGTTGACAGTGAGTGCTGCCCAGAAACCCCGGCCGTCCAGCGGGAACCTATTG  3033
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Db    814  ||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    781  ggctctggggtatggctcgggggagggggtcagggggcggctcagggggcaaa      840
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    874  GGCTCTGGGGGTATGGGCTGGCTCGGGGGAGGGGGCGGGTCAGGGGCGGCTCAGGGGCAAA   933

Qy    841  gggaaagaggctgtcctgctgtcgctgaagccgttaccagacaatgagtatcctg    900
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Db    934  GGGAAAGAGGAGGCTGTCCTGCTGTCGCTGAAGCCCGTTACCAGACAATGAGTATCCTG   993

Qy    901  cccatggagctatataaggagttgcagaatatgtgaccaccactaccgcatgctcatgt   960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    994  CCCATGGAGCTATATAAGGAGTTTGCAGAATATGTGACCAACCACTACCGCATGCTGTGT  1053

Qy    961  gccgtgctggagccgccgccctcaatgtcaaggcaaggaggagtcgtagtgcactgtt   1020
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Db   1054  GCCGTGCTGGAGCCGCCGCCCCTCAATGTCAAGGGCAAGGAGGAGTCGTTCGTAGTGCACTGTT  1113

Qy   1021  cacatcctgcaaagcacaggccaaggacttccttcagacatggccatgtcagag     1080
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Db   1114  CACATCCTGCAAAGCACAGGCACAGGCCAAGGACTTCCTTCTTCAGACATGGCCATGTCAGAG   1173

Qy   1081  gtagaccggtcatggagcgggaacacctcatattccgcgagaaacacgctcgccactaaa  1140
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Db   1174  GTAGACCGGTTCATGGAGCGGGAACACACCTCATATTCCGCGAGAACACGCTCGCCACTAAA  1233

Qy   1141  gccatagaagagtatatgagactgattggccagaaataccctcaaggatgccattggggag  1200
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Qy   1201  ttcatcgggctctgtatgaatctgagagaactgtgagtagaccccatcaagtgcaca    1260
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Qy   1261  gcgtccagtctggcagagcaccaggccaactcgcggatgtgctgtgagttggccctgtgc  1320
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Qy   1321  aaggtgtcaactccattgcgtgttcccgagggagctgaaggaggtgttttcatcatgg   1380
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Qy   1381  cggctgcgctgcgagagcgggggccgggaggacaattgctgacaggctgatcagcgcctcg  1440
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Qy   1441  ctcttcctgcgcctcctcgcccggccatcatgtcgccggtcgtgtttggactgatgcag   1500
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RESULT    2
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DEFINITION    Rattus norvegicus SynGAP-b mRNA, complete cds.
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VERSION       AF058790.1  GI:3722228
KEYWORDS      .
SOURCE        Norway rat.
  ORGANISM    Rattus norvegicus
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REFERENCE     1 (bases 1 to 4140)
  AUTHORS     Kim,J.H., Liao,D., Lau,L.F. and Huganir,R.L.
  TITLE       SynGAP: a synaptic RasGAP that associates with the PSD-95/SAP90
              protein family
  JOURNAL     Neuron 20 (4), 683-691 (1998)
  MEDLINE     98240917
REFERENCE     2 (bases 1 to 4140)
  AUTHORS     Kim,J.H. and Huganir,R.L.
  TITLE       Direct Submission
  JOURNAL     Submitted (09-APR-1998) Neuroscience, Johns Hopkins Medical
              Institute, 725 N. Wolfe Street, PCTB 900, Baltimore, MD 21205, USA
REFERENCE     3 (bases 1 to 4140)
  AUTHORS     Kim,J.H. and Huganir,R.L.
  TITLE       Direct Submission
  JOURNAL     Submitted (08-OCT-1998) Neuroscience, Johns Hopkins Medical
              Institute, 725 N. Wolfe Street, PCTB 900, Baltimore, MD 21205, USA
REMARK        Sequence update by submitter
COMMENT       On Oct 9, 1998 this sequence version replaced gi:3065890.
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                     RFRSADHDRARLMSPKFSHESLLSPSSAAEALELNLDEDSIIKPVHSSILGQEFC
                     FEVTTSSGTKCFACRSAAERDKWIENLQRAVKPNKDNSRRVDNVLKLWIIEARELPPK
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                     KKDKAGYVGLVTVPVATLAGRHFTEQWYPVTLPTGSGSGGMGSGGSGGGGGGSGG
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                     IGEFIRALYESEENCEVDPIKCTASSLAEHQANLRMCCELALCKVVNSHCVFPRELKE
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Qy   3121 cggactgtagcctgggtgtccaatatgcctcacctgtccgctgacatcgagagtgcacac 3180
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Qy   3361 atcctgatcagtaccaagcccgcctggagcgagcagcgcttgagcgcagcagcagcag 3420
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Qy   3837 tcccttaacgcctcttgggcgccacccatgtcaaccccactgctccattccaggaggga 3896
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Qy   3897 gagtgggaccctcagctgcctctcacccaggagaccaactacccccacacagacccctt 3956
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Query Match             98.9%;  Score 3936.2;  DB 74;  Length 4140;
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Matches 3944;  Mismatches  13;  Indels  0;  Gaps  0;
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Qy    85  atcaaacgtacaaagtcacaaccaaacttgaccgaccagcagctttcgacagatcctg    144
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Db   424  GATGAAGACTCCATTATCAAGCACAGTACACAGACTCCAGTCCTGGGCCAGGAGTTCTGCTTT  483

Qy   325  gaggtaacaacatcgtctgacaaatgtttgcctgtcgtctgcagccgaaaggac        384
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Qy   385  aaatgattgagaactcatcagagaggctgtgaaacccaacaagacagcccgcgggta     444
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Qy   445  gataacgtgctgaaactatggatcatagaagctcgagaggctgccccccagaagagccctca   504
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Qy   685  ggctacgttggcctggtgactggccacctgtccagtgccgcgcgctcacacagag        744
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Qy   805  ggaggaggggtcaggggcgctcaggggaaaggaggctgtcctgctgtg             864
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Db   964  GGAGGAGGGGTCAGGGGCGCTCAGGGGGCAAAGGGAAAGGAGGCTGTCCTGCTGTG     1023

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Qy  1405  cgggaggacattgctgacaggctgatcagcgctgtctgcagggtaccccagatagcagaccta   1464
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Qy  1705  ggctacatagactggccgcgagctctccacacttcacgcccctgcctctgggggtgctg    1764
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Qy  1945  cgggacctcaacagctcatcgacccttcagtgctcgaggcctcaacagctct          2004
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Db  2104  CGGGACCTCAACAGCTCCATCAACTCCTTCAGTGCTCGAGGCCTCAACAGCTCT        2163

Qy  2005  atggacatggctgctcctccctccccccaccaggaaaccgcgcccctccggt          2061
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Qy  2125  tgcacgagcagctggacatgtcagacatcacacagaggccggttgtgagtgctgaacaagagt   2184
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ORIGIN

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ORIGIN

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AF048976

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ACCESSION   AF048976
VERSION     AF048976.1  GI:2935447
KEYWORDS    .
SOURCE      Norway rat.
ORGANISM    Rattus norvegicus
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REFERENCE   1  (bases 1 to 4063)
  AUTHORS   Chen,H.-J. and Kennedy,M.B.
  TITLE     Identification and cloning of a novel 130 kd protein containing a
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  JOURNAL   (in) SOC. NEUROSCI. ABSTR.: 1466;(1997)
REFERENCE   2  (bases 1 to 4063)
  AUTHORS   Chen,H.-J., Rojas-Soto,M. and Kennedy,M.B.
  TITLE     A Synaptic Ras GTPase-activating protein (p135 SynGAP) inhibited by
            CaM kinase II
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 4063)
  AUTHORS   Chen,H.-J. and Kennedy,M.B.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-FEB-1998) Division of Biology, California Institute
            of Technology, 1200 E. California Blvd., MC 216-76, Pasadena, CA
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Db   1097  GGCTACGTTGGCTGGTGACTGTTCCAGTGGCCACCCTGGCTGGGCGCCACTTCACAGAG  1156

Qy    745  cagtggtaccccgtgaccctgccaacaggaagtgggggctctggggtatgggctcgggg   804
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Db   1157  CAGTGGTACCCCGTGACCCTGCCAACAGGAAGTGGGGGCTCTGGGGTATGGGCTCGGGG  1216

Qy    805  ggaggaggggggtcaggggggcggctcaggggcaaaggaaggaggctgtcctgctgtg   864
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Qy    865  cggctgaaggccgttaccagacaatgagtatcctgcccatggactatataagggagttt   924
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Db   1277  CGGCTGAAGGCCGTTACCAGACAATGAGTATCCTGCCCATGGAGCTATATAAGGAGTTT  1336

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RESULT 5
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DEFINITION Rattus norvegicus mRNA for synGAP-d, complete cds.
ACCESSION   AB016962
VERSION   AB016962.1 GI:4417206
KEYWORDS   synGAP-bl.
SOURCE   Rattus norvegicus (sub_species:Sprague Dawley) cDNA to mRNA.
  ORGANISM Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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            Rattus.
REFERENCE   1 (bases 1 to 4801)
  AUTHORS   Suzuki,T.
  TITLE   SynGAP-d
  JOURNAL   Published Only in DataBase (1999) In press
REFERENCE   2 (bases 1 to 4801)
  AUTHORS   Suzuki,T.

TITLE   Direct Submission
JOURNAL   Submitted (14-AUG-1998) to the DDBJ/EMBL/GenBank databases. Tatsuo
          Suzuki, Shinshu University School of Medicine, Department of
          Neuroplasticity; 3-1-1 Asahi, Matsumoto, Nagano 390-8621, Japan
          (E-mail:suzuki@sch.md.shinshu-u.ac.jp, Tel:+81-263-37-2683,
          Fax:+81-263-37-2725)
COMMENT   On Mar 16, 1999 this sequence version replaced gi:4239945.
          Sequence updated (09-Feb-1999).
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BASE COUNT   1043 a   1477 c   1314 g   967 t
ORIGIN

Query Match   89.9%; Score 3579.6; DB 74; Length 4801;
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Matches 3638; Conservative   0; Mismatches   14; Indels   20; Gaps   3;

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Qy     88 aaacgtacaaagtcacaaccccaaactgaccggaccagcagcttcgacagatcctgcct  147
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Db    3716  TATAGCAAGAGCGAGGACCTCTCTACAGGGTCCCTAAGCCCCCTGCGGCCTCCATCCTT  3775
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Db    4730  CCTGGCCCCCCAGCCCACCCCCCCACCCCCGGCTGCAGATCACAGAGAACGGCGAGTT  4789

Qy    3674  ccggaacaccgc  3685
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Db    4790  CCGGAACACCGC  4801
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RESULT   6
HSDJ570F3/c
LOCUS   HSDJ570F3   94770 bp   DNA   PRI   17-DEC-1999
DEFINITION   Human DNA sequence from clone RP4-570F3 on chromosome 6 contains a
               gene similar to Rattus norvegicus synaptic ras GTPase activating
               protein p135, the CICK0721Q.5 (polypeptide from patented cDNA
               Em:E06811) gene, the PHF1 (PHD finger protein 1) gene, the KNSL2
               (kinesin-like 2) gene, the gene for acyl-protein thioesterase,
               ESTs, STSs, GSSs and a CpG Island, complete sequence.
ACCESSION   AL050332
VERSION   AL050332.15 GI:6010176
KEYWORDS   HTG; cICK0721Q.5; CpG Island; finger protein; GTPase-activating
               protein; kinesin-like; KNSL2; p135; PHD; PHF1; ribosomal protein
               L12; RP112; SynGAP.
SOURCE   human.
ORGANISM   Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 94770)
AUTHORS   Mashreghi-Mohammadi,M.
TITLE   Direct Submission
JOURNAL   Submitted (17-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire,
               CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
               requests: clonerequest@sanger.ac.uk
COMMENT   On Oct 4, 1999 this sequence version replaced gi:5870478.
               This sequence has been finished according to sequence map criteria
               as follows. An attempt is made to resolve all sequencing problems,
               such as compressions and repeats, but not necessarily within known
               annotated human repeat sequence elements (e.g. Alu). Where the
               sequence is ambiguous, there is an annotation using the 'unsure'
               feature key.
               This sequence was generated from part of bacterial clone contigs of
               human chromosome 6, constructed by the Sanger Centre Chromosome 6
               Mapping Group. Further information can be found at
               http://www.sanger.ac.uk/HGP/Chr6
               During sequence assembly data is compared from overlapping clones.
               Where differences are found these are annotated as variations
               together with a note of the overlapping clone name. Note that the
               variation annotation may not be found in the sequence submission
               corresponding to the overlapping clone, as we submit sequences with
               only a small overlap as described above.
               The following abbreviations are used to associate primary accession
               numbers given in the feature table with their source databases:
               Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
               on the WORMPEP database can be found at
               http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP4-570F3 is
               from the library RPCI-4 constructed at the Roswell Park Cancer
               Institute by the group of Pieter de Jong. For further details see
               http://bacpac.med.buffalo.edu/
               VECTOR: pCYPAC2
               IMPORTANT: This sequence is not the entire insert of clone
               RP4-570F3 It may be shorter because we only sequence overlapping
               sections once, or longer because we arrange for a small overlap
               between neighbouring submissions.
               The true left end of clone RP4-570F3 is at 1 in this sequence. The
               true left end of clone ICRF6c-CB2046 is at 94671 in this sequence.
               The true left end of clone ICRF6c-CK0721Q is at 20826 in this
               sequence. The true right end of clone ICRF6c-CK0721Q is at 61562 in
               this sequence.
FEATURES   Location/Qualifiers
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               /db_xref="taxon:9606"
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Db   3776 CACAGCCACAGCTACAGTGATGAGTTTGGACCCTCTGGTACTGATTTTACCCGTCGGCAG 3835

Qy   2728 ctctcacttcaggacacacatgtctcccgcccagatcaccatcgtccc 2787
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Db   3836 CTCTCACTTCAGGACAACCTACAGCACATGCTCTCCCCGCCCAGATCACCATCGGTCCC 3895

Qy   2788 cagaggccagctccctcagggccaggagggcagtggtggggggcagtggtggggggggt 2847
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Db   3896 CAGAGGCCAGCTCCCTCAGGGCCAGGAGGGCAGTGGTGGGGCAGTGGTGGGGGGGGT 3955

Qy   2848 ggggccagccacctccctgcagaggggcaaaatctcagcagttgacagtgagtgctgcc 2907
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Qy   2908 cagaaaccccgccgtccagcggaacctattgcagtccccgaaccaagttatggtcct 2967
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Qy   2968 gcccgtccacgcaacagagcctcagcaaagagggcagcattggggcagcggggggcagc 3027
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Qy   3028 ggtgcggaggggggtggggggctcaagccctccatccaccaagcagcattccccagactcca 3087
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Qy   3088 tccacgctgaaccccagatgccggcctcggagcggactgtagcctggtgtccaatatg 3147
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Qy   3148 cctcacctgtccgctgacatcgagagtgcacacattgagcgcggaaagtacaagctgaag 3207
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Qy   3268 atccactcactgaaggaaagctacacatgtccaaccggaaagctggaagagtacgacgg 3327
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Qy   3328 aggctgctgtcccaggaagagcaagaagatcctgatgcagtaccaagccccgccctg 3387
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Qy   3448 atcattgg----------caggctgatgctggtggaggagctgcgcgggacca 3494
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Qy   3495 cccgccatgctgagccgctgcctgaacccaagagagaggctgctcaacgctca--gagag 3553
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Qy   3614 cctggcccccccagcccccaccccccgctcacagagaacggcgagtt 3673
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Query Match             23.1%;  Score 920.8;  DB 69;  Length 94770;
Best Local Similarity   91.0%;  Pred. No. 2.2e-167;
Matches  979;  Conservative   0;  Mismatches  97;  Indels   0;  Gaps   0;

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Db  1724  GCGGGGGCAGCGGTGGCGGAGGGGGTTGGGGGGCTGAAGCCCTTCCATCACCAAGCAG  1669
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            ------------------ Genome Center
            Center: Sanger Centre
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
            ------------------ Project Information
            Center project name: bA175A4
            ------------------ Summary Statistics
            Assembly program: XGAP4; version 4.5
            Sequencing vector: plasmid; L08752; 100% of reads
            Chemistry: Dye-terminator Big Dye; 99% of reads
            Chemistry: Dye-primer amersham; 0% of reads
            Chemistry: Dye-primer Big Dye; 0% of reads
            Consensus quality: 145680 bases at least Q40
            Consensus quality: 147560 bases at least Q30
            Consensus quality: 148600 bases at least Q20
            Insert size: 150756; sum-of-contigs
            Insert size: 148326; 10.8% error; agarose-fp
            Quality coverage: 6.43x in Q20 bases; sum-of-contigs Quality
            coverage: 6.54x in Q20 bases; agarose-fp
            ------------------
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 3 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *          1   54611: contig of 54611 bp in length
            *      54612   54711: gap of    100 bp
            *      54712   70293: contig of 15582 bp in length
            *      70294   70393: gap of    100 bp
            *      70394  150955: contig of 80563 bp in length
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FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /chromosome="6"
                     /clone="RP11-175A4"
                     /clone_lib="RPCi-11.1"
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BASE COUNT     39575 a   37381 c   36411 g   37389 t     200 others
ORIGIN
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RESULT 7
AL161903/c
LOCUS   AL161903 150956 bp   DNA   HTG   29-SEP-2000
DEFINITION Homo sapiens chromosome 6 clone RP11-175A4, *** SEQUENCING IN

Query Match   23.1%;   Score 920.8;   DB 70;   Length 150956;

Best Local Similarity   91.0%;   Pred. No. 1.9e-167;
Matches 979;   Conservative   0;   Mismatches   97;   Indels   0;   Gaps   0;

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Qy   1997  acagctctatgacatggctggctccctcccccaaccaagagaaccccgccgcccc  2056
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Db  99893  ACAGCTCTATGACATGGCTGCCTCGCCTCCCCTCCCAACCAAGGAAAAGCCACCCCCACCAC  99834

Qy   2057  ctcccgtggggtaaagacctgttctatgtagccggcaccactggccggtcctccc  2116
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Db  99833  CGCCTGGTGGTGGTAAAGACCGTTCTATGTAAGCCGGTCCACCCCCCTGGCCCGGTCCTCAC  99774

Qy   2117  cagcatactgacgagcagctcggacatcacagagccggagcagaagatgctgagtgtca  2176
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Db  99773  CAGCATACTGACGACGAGCAGCTCGGACATCACAGAGCCAGAGCAGAAGATGCTGAGTGTCA  99714

Qy   2177  acaagagtgtccatgctggacctgcagcagggcgacagggccgcctaacagca  2236
                 ||||||||||| |||| | | |||||| ||||||| || ||||||||
Db  99713  ACAAGAGTGTCCATGCTGGACTTACAGGGTGATGGCCGCCTCAACACGCA  99654

Qy   2237  gtagtgtttccaactggcagctgttgggacctgtgcactcaaccaggcttcactga  2296
                 ||||||||||||||||| ||| |||||||||||||||||||||||| ||
Db  99653  GCAGTGTTTCGAACCTGGCGGCGTGGGGCGTAGGGGACTTGCTGCACTCAAGCCAGGCCTCGCTGA  99594

Qy   2297  cagcagccttggggttgcggctgcactgccgggcggcctctcccaggggagtggctctt  2356
                 |||||||||||| || ||||| ||||| |||||| ||||||| |||||||||||||
Db  99593  CAGCAGCCTTGGGGTACGGCCTACGGCCTGCCCGGCGACCCCTCTCCCAGGGGAGTGGCTCAT  99534

Qy   2357  ccatcacagcagccggcatgccgtcagcccagatgggtgtcactacggatggtgtccccg  2416
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Db  99533  CCATCACGCGGCGGCCGTGGCATGCGCCGCCTCAGCCAGATGGGTGTCACCACGACGGTGTCCCTG  99474

Qy   2417  cccagcaactgcgcatccctctttccttccagaacccctctcttccatatggctgccgatg  2476
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Db  99473  CCCAGCAACTGCGAATCCCCCTCCTTCCTTCCAGAACCCTCTCTTCCACATGGCTGCTGATG  99414

Qy   2477  gaccaggccccccagcaggagagggagcagtgccatggtccaccttcctccccatc  2536
                 | |||||||||||| ||||||||||||| |||| |||| ||||||||||||||
Db  99413  GGCCAGTGCCCCCAGGCGGCGGGGGTGGGCCATGGCGGGGGTCCATGGGCCATGGACCCTTCCTCCCCATC  99354

Qy   2537  acaccacaccaccatcaccaccgaggggagaacccccaggggacactttgccc  2596
                 |||||||||||||||||||||||||||||||| || |||| ||||||| |||||
Db  99353  ACCACCACCACCACCACCACCGAGGGTGGAGAGCCCCCTGGGGACACCTTTGCCC  99294

Qy   2597  cgttccatggctatagcaagaggagacctctcacaggggtccctaagcccctgcgg  2656
                 | ||||||||||||| ||| || ||||||||| |||| |||||| |||||||||
Db  99293  CATTCCATGGCTATAGCCAAGAGTGAGGAGACCTCTTCCGGGTCCCAAGCCCCCTGCTG  99234

Qy   2657  cctccatccttcacagccacagctacagtgatgagtttggaccctctgtgactgatttta  2716
                 ||||||||||||||||||||||||||||||| |||||| || |||||||||| |||||
Db  99233  CCTCCATCCTTCATAGCCACCACCACAGTACAGTGATGAGTTTGGACCCTCTGGCCACTGAACTTCA  99174

Qy   2717  ccgtcggcagctctcacttcaggacaacctacagacatgtctcccgcccccagatca  2776
                 ||||| || ||||| |||||||| || |||| |||||||| || |||||||||| ||
Db  99173  CCCGTCGGCAGTTTCACTCCCAGGACACAACCTGCAGCACATGCTGTCCCCTCCCCCAGATCA  99114

Qy   2777  ccatcggtcccagaggccagctccgtcccatccagggcaggggcagtggtggggggcagtg  2836
                 |||||||||||||||| ||||| ||| |||||| ||||| |||| ||||||||||||
Db  99113  CCATTGGTCCCCAGAGGCCAGGGCCTGGAGGTGGGGGGCAGGGGTCGGGGGCGGGCAGCG  99054

Qy   2837  gtgggggcggtgggggcggggggccagcacctccttgacagcaaatctcagcagttgacag  2896
                 || ||| ||||||||||||||||||||| ||| ||||||||||||||| |||||||||
Db  99053  GTGGGGGTGGGGGGCAGGGGGCAGCCGCGCTTCCATTGCAGGGGGCAAGTGCAGCAGTTGACAG  98994

Qy   2897  tgagtgctgcccagaaacccggccgtccagcgggaacctattgcagtcccgggaaccaa  2956
                 |||||||||||||||||||||| || |||| ||||| ||||||| ||||||||||||
Db  98993  TCAGCCGCCAGCAGTTTCACTCCCAGGGACATTCCAGCCGGGGGAATCTATTGCAGTCCCCAGAGCCAA  98934

Qy   2957  gttatggtctgccgtccgtccacggcaacagagctcagcaaagaggcagcattgggggca  3016
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Db  98933  GTTATGGCCGTCCCCAGAGGCCGCGCCGCCCCCGTCCACAGGCAACAGAGCCTCGCGCAGCGGGGCA  98874

Qy   3017  gcggggcagcggtggcggagggggtggggggctcaagccctccatcaccaagcag  3072
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         80765     83307: contig of 2543 bp in length
*  83308  83407: gap of        100 bp
*  83408  88383: contig of 4976 bp in length
*  88384  88483: gap of        100 bp
*  88484  93697: contig of 5214 bp in length
*  93698  93797: gap of        100 bp
*  93798  99354: contig of 5557 bp in length
*  99355  99454: gap of        100 bp
*  99455  111055: contig of 11601 bp in length
*  111056  111155: gap of      100 bp
*  111156  118645: contig of 7490 bp in length
*  118646  118745: gap of      100 bp
*  118746  122421: contig of 3676 bp in length
*  122422  122521: gap of      100 bp
*  122522  132468: contig of 9947 bp in length
*  132469  132568: gap of      100 bp
*  132569  137959: contig of 5391 bp in length
*  137960  138059: gap of      100 bp
*  138060  151691: contig of 13632 bp in length
*  151692  151791: gap of      100 bp
*  151792  158253: contig of 6462 bp in length
*  158254  158353: gap of      100 bp
*  158354  169323: contig of 10970 bp in length.

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Query Match          23.1%;    Score 920.8;    DB 70;    Length 169323;
Best Local Similarity   91.0%;    Pred. No. 1.9e-167;
Matches 979;    Conservative   0;    Mismatches 97;    Indels   0;    Gaps   0;

Qy   1997  acagctctatggacatggctcgctccccctcccaccaaggagaaccccgccgcccc  2056
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Db  83616  ACAGCTCTATGGACATGGCTCGCCTCCCTCCCCACCAAGGAAAAGCCACCCCCACCAC  83675

Qy   2057  ctcccggtggggtaaagacctgttctatgtgagccggccaccactggccggtcctccc  2116
           ||||| |||||||||||| ||||||||||||  ||||||||||||||||||||||||
Db  83676  CGCCTGGTGGTGGTAAAGACCTGTTCTATGTAAGCCGTCCACCCCTGGCCGGTTCCTCAC  83735

Qy   2117  cagcatactgcagcagcaggacatcacagagccggacagagaaatgctgagtgtca  2176
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Db  83736  CAGCATACTGCACGAGCAGCTCGGACATCACAGAGCCAGAGACAGAAGAGATGCTGAGTGTCA  83795

Qy   2177  acaagagtgtgtccatgctgacctgcagggtcgacgggccgacgggccgcctaacagca  2236
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Db  83796  ACAAGAGTGTGTCCATGCTGACTTACAGGGTGATGGGCCTCGTGGCGCCTTCAACAGCA  83855

Qy   2237  gtagtgtttccaacctggcagctgttgggacctgttgcactcaagccaggcttcactga  2296
           ||||||||| ||||||||||||| || ||||||||||||||||||  ||| ||||||
Db  83856  GCAGTGTTTCGAACCTGGCAGCCGTAGGGGACCTGCACTCAAGCCAGGCCTCGCTGA  83915

Qy   2297  cagcagcctggggttggcggctgcactcgcggggcgcctccccaaggagtggctctt  2356
           ||||||||| |||||||  ||||||||| ||||||||||||||||||| |||| | |
Db  83916  CAGCAGCCTTGGGGGTTGGGGCTACGGCCTGCGGCGAGCCTCTCTCCCCAGGGGAGTGGCTCAT  83975

Qy   2357  ccatcacagcagccggcatcgcctcagccagccagatgggtgtcactacggatggtgtccccg  2416
           | |||||||| |||||||||||||||  ||||||||||||||||||||||||||| |||||
Db  83976  CCATCACGCGGCGCTGGCATCGCCTCAGCCCTCAGCCAGATGGTGTCACCACAGACGGTGTCCCTG  84035

Qy   2417  cccagcaactggcgcatccctctttcttccgagaccctcttccatatggctgccgatg  2476
           | |||| |||||||||||  |||||||||  |||||||| ||||||||  |||||||||
Db  84036  CCCAGCAACTGCGAATCCCCTCTCTTTCCAGAACCCTCTCTTCCACATGGCTGCTGATG  84095

Qy   2477  gaccagggccccagcaggccatggaggagcagtggccatggtccaacttcctcccatc  2536
           | |||| ||||||| |||||||||||||||||||| ||||||||  |||||||||||
Db  84096  GGCCAGGTCCCCCAGGCCGGCCATGGAGGGGCGGTGGCCCATGGTGGCCCATTCCTCCCCATC  84155

Qy   2537  accaccaccaccaccatcaccatcaccgaggggggacacttttgccc  2596
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Db  84156  ACCACCACCACCCATCACCACCACCACCGAGGTGGAGAGCCCCCTTTGCCC  84215
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KDNCRRAENVLRLWIIEAKDLAPKKKYFCELCLDDTLFARTTSKTKADNIFWGEHFEF
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EVFASWKQQCLNRGKQDISERLISASLFLRFLCPAIMSPSLFNLMQEYPDRTSRFLT
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IDLGRELSVLHSLLWEVVSQLDKGENSFLQATVAKLGPLPRVLADITKSLTNPTPIQQ
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TQVASIKQLRETQSTPQSAPQVRRPLHPALNQPGGLQPLSFQNPVYHLNNPIPAMPKA
SIDSSLENLSTASSRSQSNEDFKLSGPSNSSMEDFTKRSTQSEDFSRRHVPDRHIP
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GSRSRQQSSSRESPVPKVRAIQRQQTQQVQSPVDSATMSPVERTAAWVLNNGQYEED
VEETEQNLDEAKHAEKYEQEITKLKERLRVSSRRLEYERRLLVQEQQMKLLLEYKA
RLEDSEERLRRQQEKDSQMKSIISRLMAVEEELKKDHAEMQAVIDAKQKIIDAQEKR
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BASE COUNT     1292 a     1022 c     1012 g     1042 t
ORIGIN

Query Match                15.8%;        Score 629.4;   DB 10:    Length 4368;
Best Local Similarity      62.5%;        Pred. No. 4.3e-111;
Matches 1080;  Conservative     0;  Mismatches 571;  Indels   78;  Gaps    3;

Qy     52 caaggcttcctgagccggaggctaaaaagctccatcaaacgtacaaagtcacaacccaa 111
          |||||| ||| ||| |||| |||||||| || ||  | |  |||| ||  ||||
Db    243 CCAGGATTCTTCAGCAAGCGCCTGAAAGGCTCCATCAAGAGGACCAAAAGCCAGTCAAAG 302

Qy    112 cttgaccggaccagcagtttcgacagatcctgcccgcttccgaagtgctgaccatgac 171
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Db    303 CTTGACAGAAACACGAGCTTTCG--------GCTTCCATCCCTTGCAGTACAGATGAC 353

Qy    172 cgggccggctgatgcagagcttcaaggagtctcactccatgagtccctgctgagtccc 231
          |||| ||  | ||| | |||  |  |||| |    | |||||||| ||||| || ||
Db    354 AGGTCTCGTGGGCTGCCTAAACTAAAAGAGTCACGTTCCCATGAATCCTTGCTGAGCCCA 413

Qy    232 agcagtgctgctgaggccctggagctcaacctggatgaagatccaacattatcaagccagta 291
          ||| || ||  | ||| ||  || | |  ||| |||||| |||  ||||| ||  ||||
Db    414 TGCAGCACAGTGGAATGCTCTGGATCTTGGTAGAGGGAACCTGTATCAGTGAAACCACTT 473

Qy    292 cacagctccatcctggccaggagttctgctttgaggtaacaacatcgtctggacaaa 351
          || |||| | | |||| ||||| | || ||  |||| ||||||||  |||||| |
Db    474 CATAGTAGCATCCTTGGACAAGACTTCTGCTTGAGGTTACCTACTTAAGTGGAAGTAAA 533

Qy    352 tgtttgcctgcgtctgcagccgaaaggacaaatggattgagaatctacagagggct 411
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Db    534 TGCTTCAGCTGTAATTCTGCTTCTGAGAGACGAACAAGTGGATGGAAAACCTTCGCAGGACA 593

Qy    412 gtgaaacccacaaggacaacagcgccgggtagataacgtgctgaaactatggatcata 471
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Db    594 GTTCAACCTAATAAGGACAATTGCAGGCGAGCTGAAAATGTTCTTCGTTTATGGATCATT 653

Qy    472 gaagctcgagagctgccccccaagagagctgatattactgcgagttatgcctggacgacatg 531
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Db    654 GAAGCCAAGGACCTTGCCCCTAAAAAGAAAATATTTCTGCGAACTGTGCCTTGATGATACC 713

Qy    532 ctctatgcacggaccacttccaagcccggctcagcctcaggagacactgtctttgggc 591
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Qy    592 gagcacttgagtttaacaacctgcctgctgtccgggcgctcggcgtcatcgtaccgt 651
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Qy    652 gactcggacaaaaagcggaagaggacaaggcaggccacgtttccggttcca 711
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Db    825 GATGTGGAAAAAAAGAAGAAAAAGGACAAGAATAATTATGTAGGCTAGTCAACATCCCC 884

Qy    712 gtggccaccctgggcgccacttcacagacgcatggtaccccgtgaccctgccaaca 771
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Db    885 ACTGCCAGTGTGACTGGTCGCCAATTGTAGAAAAGTGGTATCCAGTGAGTACACCTACA 944
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Qy   2597 cgtccatggctatagcagcaggacctctctacagggtccctaagcccctgcgg 2656
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Qy   2657 cctccatccttcacagccacagctacagtgatgagtttggaccctctggtactgattta 2716
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Db  84276 CCTCCATCCTTCATAGCCACCACCACAGTGATGAGTTTGGACCCTCTGGCACTGACTTCA 84335

Qy   2717 ccgtcggcagctccacttcaggacaacctacagacatgtctccccgcccagatca 2776
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Db  84336 CCCGTCGGCAGCTTTCACTCCAGGACAACCTGCACTGCTGTCCCCTCCCCAGATCA 84395

Qy   2777 ccatggtcccagaggccagctcctcaggcgccaggagggggcaaatctcagcagttgacag 2836
          |||| | |||||| ||||| | || |||| || ||||  | | || |||| |||  |||
Db  84396 CCATTGGTCCCCAGAGGCCAGCTCCTCAGGCCTGAGTTGGAGCCGGTGGGGGCAGCG 84455

Qy   2837 gtggggcggtggggcggccagccacctccgttccaggcgcaaatccagcagttgacag 2896
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Db  84456 GTGGGGGTGCGGGGGCCAGCCGGGCCAGCGGCCAAGTCTCAGCAGTTGACAG 84515

Qy   2897 tgagtgctgcccagaaacccggccgtccagcgggaacctattgcagtcccggaaccaa 2956
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Qy   2957 gttatggtccgtgccgtcacacggcaacagagctcagcaagagggcagcattggggca 3016
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Qy   3017 gcggggcagcggtggcgaggggtggggggctcaagccctccaccaccaagcag 3072
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ACCESSION   AF047711
VERSION     AF047711.1  GI:4105588
KEYWORDS    .
SOURCE      human.
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REFERENCE   1  (bases 1 to 4368)
  AUTHORS   Noto,S., Maeda,T., Hattori,S., Inazawa,M., Asaka,M. and
            Hatakeyama,M.
  TITLE     A novel human RasGAP-like gene that maps within the prostate cancer
            susceptibility locus at chromosome 1q25
  JOURNAL   FEBS Lett. 441 (1), 127-131 (1998)
  MEDLINE   99093006
REFERENCE   2  (bases 1 to 4368)
  AUTHORS   Noto,S., Maeda,T., Hattori,S. and Hatakeyama,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-FEB-1998) Department of Viral Oncology, The Cancer
            Institute, Japanese Foundation for Cancer Research, 1-37-1
            Kami-Ikebukuro, Toshima-ku, Tokyo, Japan
FEATURES             Location/Qualifiers
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                     /map="1q24"
     CDS             126..3545
                     /note="ras GTPase activating protein"
                     /codon_start=1
                     /product="nGAP"
                     /protein_id="AAD04814.1"
                     /db_xref="GI:4105589"
                     /translation="MQTPEVPAERSPRRRSISGTSTSEKPNSMDTANTSPFKVPGFFS
                     KRLKGSIKRYKSQSKLDRNYSFRLPSLRSTDDRSRGLPKLKESRSHESLLSPCSTVEC
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ACCESSION   AF053938
VERSION     AF053938.1  GI:3213253
KEYWORDS    .
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1 (bases 1 to 829)
  AUTHORS   Chen,H.-J. and Kennedy,M.B.
  TITLE     Identification and cloning of a novel 130 kd protein containing a
            ras GTPase-activating domain from the rat forebrain postsynaptic
            density
  JOURNAL   Abstr. - Soc. Neurosci. 23, 1466-1466 (1997)
REFERENCE   2 (bases 1 to 829)
  AUTHORS   Chen,H.J., Rojas-Soto,M., Oguni,A. and Kennedy,M.B.
  TITLE     A synaptic Ras-GTPase activating protein (p135 SynGAP) inhibited by
            CaM kinase II
  JOURNAL   Neuron 20 (5), 895-904 (1998)
  MEDLINE   98282016
REFERENCE   3 (bases 1 to 829)
  AUTHORS   Chen,H.-J. and Kennedy,M.B.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-MAR-1998) Biology, California Institute of
            Technology, 1200 E. California Blvd., MC 216-76, Pasadena, CA
            91125, USA
FEATURES             Location/Qualifiers
     source          1..829
                     /organism="Rattus norvegicus"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
     CDS             183..>829
                     /note="synaptic ras GTPase-activating protein; N-terminal
                     splice variant; synaptic ras-GAP"
                     /codon_start=1
                     /product="p135 SynGAP"
                     /protein_id="AAC23491.1"
                     /db_xref="GI:3213254"
                     /translation="MGLRPTPTPSGGSGSGSLPPPSHRQPLRRRCSSCCFPGEYHLG
                     RSRRKSVPGGKQYSMEAAPAPFRPSQGFLSRRLKSSIKRTKSQPKLDRTSSFRQILP
                     RFRSADHDRARLMQSFKESHSHESLLSPSSAAEALENLDEDSIIKPVHSSILGQEFC
                     FEVTTSSGTKCFACRSAAERDKWIENLQRAVKPNKDNSRRVDNVLKLWIIEARELP"
BASE COUNT      182 a    266 c    218 g    163 t
ORIGIN
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Query Match             11.1%;  Score 443.2;  DB 74;  Length 829;
Best Local Similarity   97.2%;  Pred. No. 3.7e-75;
Matches  451;  Conservative  0;  Mismatches  13;  Indels  0;  Gaps  0;

Qy     25 gcaccccatttccccattgctccccagcaaggcttctgagccggaggctaaaaagctcc    84
          ||||| ||  ||||| | ||||||  |||| ||| ||||||||||||||||||||||||||
Db    366 GCCCCCGCTGCGCCCTTCCGGCCCTCCAAGGCTTCCTGAGCCGGAGGCTAAAAAGCTCC   425

Qy     85 atcaaacgtacaaagtcacaaccaaactgacggacaacagagagctttcgacgatcctg   144
          ||||||||||||||||||||||||||||||||||||||||||||||| ||||| |||||
Db    426 ATCAAACGTACAAAGTCACAAGTCACAACCCAAACTTGACCGGACCAACAACCAGATCCTG   485

Qy    145 cctcgcttccgaagtgctgaccatgaccgggcccggctgatgcagagcttcaaggaggtct  204
          |||||||||||| ||||||||  ||||||||||||||||||||||||||||||||||| ||
Db    486 CCTCGCTTCCGAAGTGCTGACCATGCTGACCATGCCGGGCCGGCTGATGCGAGAGCTTCAAGGAGTCT   545

Qy    205 cactccccatgagtccctgctagtcccagcagtgtctgctgctgaggctcaacctg   264
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    546 CACTCCCATGAGTCCCTGCTGAGTCCCAGCAGTGCTGCTGCTGGAGCTCAACCTG   605

Qy    265 gatgaagactccattatcaagccagtacacagctccatcctggccaggagttctgcttt   324
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    606 GATGAGACTCCATTATCAAGCCAGTACACAGCTCCATCCTGGGCCAGGAGTTCTGCTTT   665

Qy    325 gaggtaacaacatcgtctgggacaaaatgttttgcctgtcggttctgcagccgaaaggac   384
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    666 GAGGTAACAACATCGTCTGGGACAAAATGTTTTGCCTGTCGGTCTGCAGCCGAAAGGGAC   725
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Qy    772 ggaagtgggggctctcggggggtatgggctcggggggaggagggggtcagggggcgctca    831
          ||||| ||||||||||||||||||||||||||| || ||
Db    945 CCCAA------------------------------------------------------    949

Qy    832 ggggcaaaggaaaggaggcgtcctgctgcggctgaaggcccgttaccagacaatg    891
          ||||||  ||  ||  || |||||| |||  |||| || ||   ||  |||
Db    950 ----CAAAGGAAAGACAGGAGACCTTCTATTCGGATTAAATCACGTTTCCAAACTATC   1004

Qy    892 agtatcctgccatggagctataagggagtttgcagaaatagtgaccaaccactaccgc    951
          || ||||||||||||||| ||| | ||||| ||||||  ||| ||||||||||||||
Db   1005 ACCATTCTGCCTATGGGAGCCAGTAATTAGTGTGAGAAATAAAGAGGAGTTGGCTTGT   1064

Qy    952 atgctgtgcgtgctggacgccgccctcaatgtcaaggcaaggaggagtcgctagt   1011
          |||||||| || ||||||||   |||||| |||||||| | |||
Db   1065 ATGCTGTGTCGTCCTTGAGCCAGTAATTAGTGTGAGAAATAAAGAGGAGTTGGCTTGT   1124

Qy   1012 gcactggttcacatcctgcaaagcacaggcaaggcaaggacttcctttcagacatggcc   1071
          || | ||  |||||||||||||| |  ||  ||||   |||||| | ||| |||
Db   1125 GCCTTAGTGCACCATTCTTCAAAGTACTGGCAGAGGCCAAGGAGTTTTCTGACTGCTTGTG   1184

Qy   1072 atgtcagaggtagaccggttcatggagcgggaacacctcatattccgcgagaacacgctc   1131
          ||||| | || |  |  |||||| | |||||| ||| | |||| ||  ||| || |  ||
Db   1185 ATGTCTGAGGTGGATCGTGTGGAGCGGGAGCATGATGTTGGGACATCGGAGAGAACACTATT   1244

Qy   1132 gccactcaaagccatagagagtatatgagactgattggccagaaatacctcaaggatgcc   1191
          ||||| ||  ||||  ||| ||  |||  |||   | | ||||  |  | |  ||||||
Db   1245 GCCACCAAATCCATTGAGGAATACCTCAAGTTGGTGGGACAACAGTATCTTCATGACGCA   1304

Qy   1192 attggggagttcatccggggtctgtatgaatctgagagaactgtgaagtagacacccatc   1251
          | |||||| ||||| || | | || || |  |||| |||||||  || |  |  ||
Db   1305 CTGGGGGAGTTTATCAAAGCTTGTGTATGAGTCGATGAGAACTGTGAAGTGCATCCCAGC   1364

Qy   1252 aagtgcacagcgtccagtctgcagagcaccagccaacctgcgcatgtgctgtgagctg   1311
          ||  ||||| ||| | |||   || || ||||| |||||||||||| ||| |||||
Db   1365 AAATGTTCATCTAGTGAACTGATAGAGCCCATGAACCAGAGCAACCTGAAAATGTGCTGTGAGCTG   1424

Qy   1312 gccctgtgcaaggtgtcaacctccattgcgtgttcccgagggagctgaagaggagtgttt   1371
          ||| | |  | |||||||||  |   |||   || ||| || ||  ||||  ||
Db   1425 GCTTCTGCAAGATCATCAACTCTTACTGTGTTTTCCCTCGTGAGTTGAAAGAAGTGTTT   1484

Qy   1372 gcatcatggcggctcgctgtgcagagcgggcgggcggggaggacattgctgacaggctgatc   1431
          |||  | | | | |  |||  |   || || || || || || ||||||| ||||||||
Db   1485 GCATCATGGAGGCAGCAGTGCGTGCAACCGTGCAAGCAAGATCAGCGAGAGGCTCATC   1544

Qy   1432 agcgcctcgcttcctgcgcttcctgcgccggcatcatgtcgcccagtcgtgttgga   1491
          || || |  | || |||||| | ||||| || | ||  |||||||  ||  || ||
Db   1545 AGTGCCTCATTATTCTCCGTTTCTCCGTGTCCAGCCATTATGTCTCCCAGTCTTTTCAAC   1604

Qy   1492 ctgatgcaggagtaccaagatgagcagacccctcacggaccctcatcgccaaggtt   1551
          || ||||| |||| |  | |||| | ||||  | || ||  |  || |  |||
Db   1605 CTTATGCAGGAGTATCCGAATGACCGGCACATCTGATGGACTCTTAACTCCTTATTGCCAAGGTC   1664

Qy   1552 atccagaacctggccaactttcacaagttacctcaaaggaggagacttcctgggcttcatg   1611
          |  || |  ||||||  || |||||||||||  ||||||| || |  |
Db   1665 ATTCAGAACCTGGCCAACTTTCCCAAGTTACCTCAAAGGAGGAATACATGGCATTCATG   1724

Qy   1612 aacgagtttctggagctgaataggggttctatgcagcaattcctgtatgagatatccaac   1671
          ||  || ||||||||| || |  || |  |||||  |   |  | || |   |
Db   1725 AATGATTTTTAGAACATGAATGGGTGGAATGAAGCGCTTTCTTTTGGAGATCTCTAAT   1784

Qy   1672 ctggacacactgaccaacagcagagtttgaggggctacatagacttgggccgcgagctc   1731
          ||  |   |  ||||||  |  |||||| || || |    || |  | | |
Db   1785 CCAGACACCATCTCAAACACCCCAGGCTTTGATGGTTACATTGATCGGGCCGGAGAGCTTT   1844

Qy   1732 tccacacttcacgccctgctctgggaggtgctgccccagctcagcagg   1780
          ||  | |  | | |  ||| | ||| || || |
Db   1845 TCAGTTTGCATTCCTTACTGTGGGAAGTAGTTTCCCAACTTGATAAGG   1893
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RESULT 10
AF053938
LOCUS       AF053938     829 bp    mRNA              ROD       12-JUN-1998
DEFINITION  Rattus norvegicus p135 SynGAP mRNA, partial cds.
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Qy    385  aaatggattgagaattctacagagggctgtgaaaccaacaaggacaacagccgccgggta  444
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    726  AAATGGATTGAGAATTCTACAGAGGGCTGTGAAACCAACAAGGACAACAGCCGCCGGGTA  785

Qy    445  gataacgtgctgaaactatggatcatagaagctcgagagctgcc  488
           ||||||||||||||||||||||||||||||||||||||||||||
Db    786  GATAACGTGCTGAAACTATGGATCATAGAAGCTCGAGAGCTGCC  829

RESULT 11
AK024488
LOCUS       AK024488      4287 bp    mRNA           PRI       29-SEP-2000
DEFINITION  Homo sapiens mRNA for FLJ00087 protein, partial cds.
ACCESSION   AK024488
VERSION     AK024488.1  GI:10440489
KEYWORDS    fis (full insert sequence).
SOURCE      Homo sapiens adult spleen cDNA to mRNA, clone:as00087.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4287)
AUTHORS     Ohara,O., Nagase,T., Kikuno,R. and Okumura,K.
TITLE       The nucleotide sequence of a long cDNA clone isolated from human
            spleen
JOURNAL     Published Only in DataBase (2000) In press
REFERENCE   2  (bases 1 to 4287)
AUTHORS     Ohara,O., Nagase,T., Kikuno,R. and Okumura,K.
TITLE       Direct Submission
JOURNAL     Submitted (24-AUG-2000) to the DDBJ/EMBL/GenBank databases. Osamu
            Ohara, Kazusa DNA Research Institute, Department of Human Gene
            Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan
            (E-mail:cdnainfo@kazusa.or.jp, URL:http://www.kazusa.or.jp/NEDO,
            Tel:81-438-52-3913, Fax:81-438-52-3914)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            International Trade and Industry of Japan; cDNA full insert
            sequencing: Research Association for Biotechnology; cDNA library
            construction, 5'- & 3'-end one pass sequencing and clone selection:
            Kazusa DNA Research Institute.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="as00087"
                     /dev_stage="adult"
                     /tissue_type="spleen"
                     /note="vector:pBluescriptII SK plus"
     gene            1339..3363
                     /gene="FLJ00087"
     CDS             <1339..3363
                     /gene="FLJ00087"
                     /note="For this clone, GeneMark analysis triggered an
                     alert for spurious CDS split. The result of GeneMark
                     analysis of the nucleotide sequence of this clone is
                     accessible through http://www.kazusa.or.jp/NEDO.
                     Start codon is not identified."
                     /codon_start=1
                     /product="FLJ00087 protein"
                     /protein_id="BAB15778.1"
                     /db_xref="GI:10440490"
                     /translation="GSTLHLRCLLWGANKPKRFPPSHSHLQDNVEREETWLSVWVHEA
                     KGLPRAAAGAPGVRAELWLDGALLARTAPRAGPGQLFWAERFHFEALPPARRLSRLIR
                     GLGPGSAVLGRVALALEELDAPRAPAAGLERWFPLLGAPACGAALRARIRARRLRVLPS
                     ERYKELAEFLTFHYARLCGALEPALPAQAKEELAAAMVRVLRATGRAQALVTDLGTAE
                     LARCGREALLFRENTLATRAIDEYMKLVAQDYLQETLGQVVRRLCASTEDCEVDPSK
                     CPASELPEHQARLRNSCEEVFETIIHSYDWFPAELGIVFSSWREACKERGSEVLGPRL
                     VCASLFLRLLCPAILAPSLFGLAPDHPAPGARTITLIAKVIQNLANRAPFGEKEAYM
                     GFMNSFLEEHGPAMQCFLDQVAMVDVDAAPSGYQGGGDLALQLAVLHAQLCTIFAELD
                     QTTRDTLEPLTILRAIEEGQPVLVSVPMRLPLPPAQVHSSLSAGEKPGFLAPRDLPK
                     HTPLISKSQSLRSVRRSESWARPRPDEERPLRRPRPVQRTQSVPVRRPARRRQSAGPW
                     PRPKGSLSMGPAPRARPWTRDSASLPRKPSVPWQRQMDQPQDRNQALGTHRPVNKLAE
                     LQCEVAALREEQKVLSRLVESLSTQIRALTEQQEQLRGLQDLDSRLRAG"
BASE COUNT      785 a    1529 c    1261 g    712 t
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ORIGIN

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Query Match              8.5%;  Score 336.4;  DB 34;  Length 4287;
Best Local Similarity   59.28%;  Pred. No. 7.7e-55;
Matches  574;  Conservative  0;  Mismatches  396;  Indels  0;  Gaps  0;

Qy    857  ctgctgtgcgctgaagcccgttaccagacaatgagtatcctgccatggactatata   916
           || ||| ||||| | ||||| || || |||||||||||| |||| || ||||| ||
Db   1769  CAGCGCTGCGCGGCGGGCGGGGCGGGGATTCGGCGCCGTGCCGTGCCGTCCGAGCGCTACA 1828

Qy    917  aggagtttgcagaatatgtgaccaaccactaccgcatgctgtgtgcgctggagccg   976
           || || ||| ||| |||  |||  | ||| |||| | |||||| | |||||||||||
Db   1829  AGGAGCGTGGCGGAGTTCCTCACCTTCCACTATGGCGCCGTCTCGCGGGCCCCTGAGCCCG 1888

Qy    977  ccctcaatgtcaaggcaaggaggagtcgtagtgcactggttcaatcctgcaaagca  1036
           ||| || | || || ||  ||| |||  || |||| ||| | ||||| || |||||
Db   1889  CGCTGCCTGCCGCAGGCCAAGGAGCTGGCGGACCATGTGCGCGTGCTGCGGGCCA 1948

Qy   1037  caggcaaggccaaggacttccttcagacatgccatgtcaggagtagaccggttcatgg  1096
           ||| | |||| || || || || || || |||| || ||| ||| ||| ||| |||||
Db   1949  CCGGGCCGGGCCAGGCGCTGGTGACTGACCTGGGCACTGCAGCTGCGGCCTGTGGAG 2008

Qy   1097  agcgggaacactcatattccgcgagaacacgctcgccactaaagccataagagagtata  1156
           || ||| |||| | |||||||| |||||||||| || ||||| ||||| ||||||||
Db   2009  GCCGTGAGGCCGTGCTTCCGGGAAAACACATTGGCACCAGGCTATCGATGAGTACA 2068

Qy   1157  tgagactgattggccagaaaatacctcaaggatgccattgggagttcatccggctcgt  1216
           || ||| || ||| || ||||||| || ||||| |||  |||  |||| ||||| |||
Db   2069  TGAAGCTCGTGGCACAGGATTACCTCCAGGAGACCCTGGGACAGGTTGTGCGGCGTCT 2128

Qy   1217  atgaatctgaggagaactgtgaagtagacccatcaagtgcacagcgtccagtcggcag  1276
           || ||| ||| ||||||| |||||||| || | ||| ||| ||| |||||||| ||||
Db   2129  GTGCTTCTACTGAGGACTGTGAAGTGACCCCAGCAAATGTCCAGCCTCGAGCTGCCAG 2188

Qy   1277  agcaccaggccaacctgcggatgtgctgtgagttggccctgcaaggtggtcaactccc  1336
           |||||||||||||| ||||| ||||| || || || |||||| |||||||| |||||||
Db   2189  AGCACCAGGCCAGACTTCGGAACAGCTCGGAGGAGGTCTTCGAAACCATTATCCATTCCT 2248

Qy   1337  attggtgttcccgaggggagctgaaggaggtgtttcatcatgcggccgctgcgctgtgcag  1396
           | ||||| ||||| || ||||| || ||||| || ||||| || | |||||| ||| |||
Db   2249  ACGACTGGTTCCCTGCGGAGCTGGGCATCGTGTTCTCAAGCTGGCGAGAAGCATGTAAAG 2308

Qy   1397  agcgggccggaggacattgctgacaggctgatcagcgcctgctctcttcctgcgcttcc  1456
           || || ||| || || |||| || |||| || |||| ||| |||| |||||||| |||
Db   2309  AACGTGGCTTCGAGGTGCTGGGCGCCCGACTGGTGTGCGCCTCCACTGAGGATTGCGAGG 2368

Qy   1457  tctgcccggccatcatgtcgcccagtctgtttggactgatgcgaggagtaccagatgagc  1516
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Db   2369  TGTGCCCTGCCATCCTGGCACCCAGCCTCTTTGGTTTGGCACCAGACCATCCAGCACCCG 2428

Qy   1517  agacctcagaacctcacctcatcgcaagttatccagaacctgccaactttcca  1576
           | ||| |||| ||| |||| || ||  || ||||||| |||| ||||| ||||
Db   2429  GCCCAGCCCGACCACCCTCACACTGATTGCCAAGGTCATCCAGAACCTGCCCAACCTGCCC 2488

Qy   1577  agtttacctcaaagaggagacttcctgggcttcatgaacgagtttctggagctggaatggg  1636
           || ||| |||| || | || ||  ||||| ||||| || ||||| |||||||| ||||||
Db   2489  CGTTCCGTGAGGAGGAGCGCTTACATGGGCTTCCTGGAGGAACATGGAC 2548

Qy   1637  gttctatgcagcaattcttgtatgagatatccaacctggacacactgaccaacagcagca  1696
           | |||| | | || || |||| ||| |  || || || ||||||| ||||| || || |
Db   2549  CAGCCAGCCAATGCTTCCTGGACCAGGTAGCCATGGTGGATGTGGATGCGCCCCCAGTG 2608

Qy   1697  gttttgagggctacatagacttgggccgcgagctctccacacttcacgccctgctctggg  1756
           || | |||| ||| | |||| |   | | |  || || ||||||||| ||||||| |||
Db   2609  GTTACCAGGGCAGTGGTGATCTGGCCCTCCAGTTAGCTGTCCTGCATGCCCAGCTCTGTA 2668

Qy   1757  aggtgctgccccagtcagcaggaagcccctcgaagtggcccccggctcc  1816
           || | || || || || || || ||  |||| || | ||||| ||||||
Db   2669  CAATTTTGCTGAGCTTGACCAGACAACCCGAGACCCCTGGAACCACTGCCACCATCC 2728

Qy   1817  tcagcgacat  1826
           | |||| |||
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Db   2729 TGCGAGGCAT 2738

RESULT 12
AC019800/c
LOCUS   AC019800   56366 bp   DNA   HTG   03-JAN-2000
DEFINITION Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
            pieces.
ACCESSION   AC019800
VERSION   AC019800.1 GI:6665097
KEYWORDS   HTG; HTGS_PHASE2.
SOURCE   fruit fly.
ORGANISM   Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1 (bases 1 to 56366)
AUTHORS   Adams,M. and Venter,J.C.
TITLE   Direct Submission
JOURNAL   Submitted (30-DEC-1999) Celera Genomics, 45 West Gude Drive,
            Rockville, MD, USA
COMMENT   This sequence was identified as CDM:10210991 by the submitter.
            For more information on this record e-mail to fly@celera.com.
            * NOTE: This is a 'working draft' sequence.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
FEATURES   Location/Qualifiers
     source   1..56366
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
BASE COUNT   16234 a 11808 c 11924 t 16400 g
ORIGIN

Query Match   6.08%; Score 240.2; DB 39; Length 56366;
Best Local Similarity   50.6%; Pred. No. 1.2e-36;
Matches 748; Conservative 0; Mismatches 683; Indels 48; Gaps 5;

Qy   376 gaaaggacaaatggattgagaatctacagagggctgaaacccaacaaggacaacagc 435
          || ||| ||| ||||||| |||| | | | ||| | ||| || | |||
Db 25786 GAGCGCGGACCTTTGGATCTACTCGCTGCGCAAGTCGATCGCTCCGAATGCAGCACACG 25727

Qy   436 cgccgggtagataacgtgctgaaactatggatcatagaagctcgagagctgcccccaag 495
          | |||| |||| |||| ||| ||| || |||| | ||||||| | ||||| |||||||
Db 25726 CGTCGCACGGACAACTCGCTGAAGATGTGGGTGTACGAGGCGAAAAATCTGCCGCCCAAG 25667

Qy   496 aagcgatattactgcgagttatgcctgaacgacatgctctatgcacgaccacttccaag 555
          ||||| || | ||||| | ||| |||| ||||| | |||| | || ||||| ||||||
Db 25666 AAGCGTTACTTTTGCGAACTGCCAATTGGACAAGACGCTGTACGGCCCGACTTCGGTGAAG 25607

Qy   556 ccccgctcagcctcaggagacactgtcttttggggcgagcacttcgagtttaacaacctg 615
          | |||| |||| | || | |||||||||||||| ||| ||||| | || | | | |
Db 25606 CTGCAGAC-------GGATCGTGCTGTTTCGGGGGGAGCACTTCGAtTTCCCCGACATA 25556

Qy   616 cctgctgtccgggcgtgcggctgcatcctgacctgtaccgtgactcggacacaaaaaagcggaagaag 675
          |||| || ||||| || | |||| |||| | |||| | || |||| |||||||||| ||| |||
Db 25555 CCCGAGATTAATGTGATCACTGTTAACGTTTTTCCGTGAGGTGACAAGAAGAAGAAGAAGCGG 25496

Qy   676 gacaaggcaggctacgttggcctggtgactgttccagtgccaccctggctgggcgccac 735
          ||||| ||||||||||||||| ||| |||| ||||| ||| ||||| |||| | |||
Db 25495 GACAAATACCAATTTGTGGGATCGGTGAAGATACCCGTGCACGATGTCCACCTCCAGATTG 25436

Qy   736 ttcacagagcagtggtaccccgtgacccctgccaacagaagtggggctctgggggtatg 795
          ||||||||| | || ||| ||||| ||||| || |||| | | ||| || |||| ||
Db 25435 CCCTTGCGAACAATGGTATCCCATA-------------CTGAGCGACAAGGCGGGC 25394

Qy   796 ggctcgggggaggaggggggtcagggggcggctcaggggcaaaggggaaagaaggaggctgt 855
          ||| |||| |||| || ||| | ||||| | | ||| ||||| | ||| | ||| | |
Db 25393 GACAGTCTGGGCAGCAGGACATCGGGCCGGCCGGCCGCAGGCCCGCAGGCTGGTCTCAAGGACACAAGGACAATTG 25334

Qy   856 cctgctgtcgcggctgaaggccgttaccagacaatgagtatcctgcccatgagctatat 915
          || || | ||| || || || ||| || ||||| | || | | ||||| || |
Db   CTACACAGTTTGCTCAGCGAAAGCCTGCCAAGCTGCCGGCCAGGCAGGCGCCCAGCTG 25834

Db   25333 CCCACGCTGAGGATCAAGTGTCGTTCCAGAGGACCAGACATCCTGCCCATCAATGTGTAC 25274

Qy   916 aaggagtttgcagaatatgtgaccaaccactaccgcatgctgtgtgcccgtgctggagccc 975
          | ||| |||||||| | | | | | ||| | || | ||| | || |||| |||
Db   25273 GGCAACTTTTTGACGTACCTCAAGGAACATAAGCGGCCTGTGCGAGACCCTGGAGCCCA 25214

Qy   976 gccctcaatgtcaaggcaagagaggagtgcagtcgtagtcgctgactggttcacatcctgcaaagc 1035
          || | || || || | ||||| |||||| || |||| | ||||| || |||||| | ||
Db   25213 GTGATCGGAGTCAAGGCCAAGGACCACATTGGACAGGACACTGGTCTGCTGATGCACGCA 25154

Qy   1036 acagcaaggccaaggacttccttcagacatggccatgtcagaggtagacgggttcatg 1095
          || | ||| | || || |||| || | | | | | |||
Db   25153 CAGGGGATTGGCGGGCGCCTTCCTCACCGATGTGTGGCCCTCCATCTGCTGCGGAGTTGGC 25094

Qy   1096 gagcggggaacactcatattccgcgagaacacgctcgccactaaagccatagaagagtat 1155
          |||| || || ||| | | | | || ||| || | | ||| | | |
Db   25093 GATCACGAGG--CTTACGTTCAGGGGACCAACTCCTTGCCCACCAAGAGCATGAGGCATTC 25037

Qy   1156 atgagactgattggccagaaatacctcaaggatgcgcattggggagttcatccgggctctg 1215
          |||| | || || || ||| | || |||| | | | | || | | | ||||
Db   25036 CTCAAGCTGACGGGCGAACAGTATCTGCAGGACACACTACTCCGCCACCAATAAACGAGCTA 24977

Qy   1216 tatgaatctgaggagagctgtgaagtagacccccatcaagtgca--------cagcgtcc 1266
          || | | |||| || | | | | | | | || | |||| | | ||
Db   24976 ATTCAGTCGGAGAGGGACTGCGAGGTGGATCCCCACCAGAGACGGGTTCGTCCGCGGGT 24917

Qy   1267 agtctggcagagcaccaggcaacctgcggatgtgctgtgagttggccctgcaaggtg 1326
          ||| |||| | |||| |||||| || | | | || | ||||| || | | |
Db   24916 TCGCTCAGCGACACAGCAGCCGCCTGCCTGCGTGCGCGGTCCGAGGGCGTGGCAGTGCATC 24857

Qy   1327 gtcaactccattgcgtgttcccgaggagctgaaggaggtgtttgcatcatggcggctg 1386
          | | || | | | | | |||| | | || | | | ||| || | ||||||
Db   24856 TTCGAATCGCACAAGCATTTCCCGCCAGTTACGAAATTGCTTTGCGACGTTCCGGGAG 24797

Qy   1387 cgctgtgcagagcgggggccgggaggacattgtgacaggctcatcagcgcctcgctcttc 1446
          ||| | | | ||| || | || ||| |||| | | ||| || | | ||||
Db   24796 CGCTTGCAGCAGCTGGGCCGTCAGGATATGGCCGTCAGACCTGATCTCGGCGAGCATTTC 24737

Qy   1447 ctgcgtcctctgccccggccatcatgcgcccagtcgttggactgatgcaggagtac 1506
          || ||| | | | ||| | |||| | | || || || | || |||||| |
Db   24736 CTGCGCTTCGTGTGCCCGGCCATCCTGTCGCCGTCGCGTCGTCCTTCAATATCACCAGCGAACTG 24677

Qy   1507 ccagatgagcagacctcacgaacctcaccctcatcgccaggttatccagaacctggcc 1566
          |||||| ||||| || | | ||| || | |||| || | |||| ||| ||||
Db   24676 CCGTCCGCACGGGCCCAATCTCACACTGGTGGCCAAGACCCTGCAAACATTGGCC 24617

Qy   1567 aacttttccaagtttacctcaaaggaggacttcctggcttcatgaacgagtttctggag 1626
          || ||||| ||| | | | | ||| |||| |||| |||| | | || ||||
Db   24616 AATTTCACCCGCTTCCAGGGCAAAGAGACTTTATGGAGTTTCCAACGATTTCCTCGAG 24557

Qy   1627 ctggaatgggttcatgcagcaattcttgtatgagatcacaactggacacactgac- 1685
          ||||| || || || || | | | | | || || | | ||| | | |||
Db   24556 CAGGAGGCCGCTCGCATGCAACACGTTTCTGGAGATTATATCCACCGGCCGGCCACCCA 24497

Qy   1686 -------caacagcagttttgagggctacatagacttggccgcgagctccaca 1737
                 || | | || ||| ||| || | || || | || || || |
Db   24496 GCTTCCAGACTCGATCCTTCGATTGGGCCCGGGTACATCGACAACAGTTGTCCATA 24437

Qy   1738 cttcacgccctgctctgggaggtgctgccccagctcagcaaggagagccctcctgaagctg 1797
          || | | | || || || ||| || |||||||| ||| | | || | |
Db   24436 CTACACAGTTTGCTCAGCGAAAGCCTGCCAAGCTGCCGGCCAGGCAGGCTG 24377

Qy   1798 ggccccgctgccccggctcctcagcgaccatcagcacagc 1836
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Db   24376 GATCCGTTGCAGCATATTCTCGATGAAATCAGCCGAGCC 24338

RESULT 13
AC012162
LOCUS   AC012162   191504 bp   DNA   HTG   09-FEB-2000
DEFINITION Drosophila melanogaster chromosome X clone BACR01N10 (D1115)
            RPCI-98 01.N.10 map 16D-16F strain y; cn bw sp, *** SEQUENCING IN
            PROGRESS ***, 142 unordered pieces.

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ACCESSION   AC012162
VERSION     AC012162.9  GI:6957580
KEYWORDS    HTG; HTGS_PHASE1.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 191504)
  AUTHORS   Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,
            Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L.,
            Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
            Hinkle,A., Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K.,
            Kearney,L., Lee,B., Lewis,S., Li,P., Ling,H., Moshrefi,A.R.,
            Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S., Pfeiffer,B.,
            Richards,S., Sethi,H., Svirskas,R.R., Wan,K.H., Webster,D.,
            Woolley,P., Yang,S., Yee,M., Yu,C. and Rubin,G.M.
  TITLE     Sequencing of Drosophila melanogaster
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 191504)
  AUTHORS   Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,
            Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L.,
            Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
            Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L.,
            Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P.,
            Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S.,
            Pfeiffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E.,
            Svirskas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and
            Rubin,G.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-OCT-1999) Drosophila Genome Center, Lawrence Berkeley
            Laboratory, MS 64-121, Berkeley, CA 94720, USA
COMMENT     On Feb 11, 2000 this sequence version replaced gi:6838825.
            For further information about this sequence, including its location
            and relationship to other sequences, please visit our sequence
            archive web site (http://www.fruitfly.org/sequence/) or send email
            to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet
            the following cutoffs: length >= 200 bases.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 142 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *         1    456: contig of 456 bp in length
            *       457    536: gap of unknown length
            *       537   1004: contig of 468 bp in length
            *      1005   1084: gap of unknown length
            *      1085   1958: contig of 874 bp in length
            *      1959   2038: gap of unknown length
            *      2039   2248: contig of 210 bp in length
            *      2249   2328: gap of unknown length
            *      2329   2858: contig of 530 bp in length
            *      2859   2938: gap of unknown length
            *      2939   3325: contig of 387 bp in length
            *      3326   3405: gap of unknown length
            *      3406   4165: contig of 760 bp in length
            *      4166   4245: gap of unknown length
            *      4246   4716: contig of 471 bp in length
            *      4717   4796: gap of unknown length
            *      4797   5373: contig of 577 bp in length
            *      5374   5453: gap of unknown length
            *      5454   6050: contig of 597 bp in length
            *      6051   6130: gap of unknown length
            *      6131   6720: contig of 590 bp in length
            *      6721   6800: gap of unknown length
            *      6801   7461: contig of 661 bp in length
            *      7462   7541: gap of unknown length
            *      7542   8104: contig of 563 bp in length
            *      8105   8184: gap of unknown length
            *      8185   8505: contig of 321 bp in length
            *      8506   8585: gap of unknown length
            *      8586   9227: contig of 642 bp in length
            *      9228   9307: gap of unknown length
            *      9308  10091: contig of 784 bp in length
            *     10092  10171: gap of unknown length
            *     10172  11099: contig of 928 bp in length
            *     11100  11179: gap of unknown length
            *     11180  11747: contig of 568 bp in length
            *     11748  11827: gap of unknown length
            *     11828  12767: contig of 940 bp in length
            *     12768  12847: gap of unknown length
            *     12848  13398: contig of 551 bp in length
            *     13399  13478: gap of unknown length
            *     13479  14007: contig of 529 bp in length
            *     14008  14087: gap of unknown length
            *     14088  14867: contig of 780 bp in length
            *     14868  14947: gap of unknown length
            *     14948  15562: contig of 615 bp in length
            *     15563  15642: gap of unknown length
            *     15643  16859: contig of 1217 bp in length
            *     16860  16939: gap of unknown length
            *     16940  17986: contig of 1047 bp in length
            *     17987  18066: gap of unknown length
            *     18067  19341: contig of 1275 bp in length
            *     19342  19421: gap of unknown length
            *     19422  20926: contig of 1505 bp in length
            *     20927  21006: gap of unknown length
            *     21007  22153: contig of 1147 bp in length
            *     22154  22233: gap of unknown length
            *     22234  23236: contig of 1003 bp in length
            *     23237  23316: gap of unknown length
            *     23317  24607: contig of 1291 bp in length
            *     24608  24687: gap of unknown length
            *     24688  25620: contig of 933 bp in length
            *     25621  25700: gap of unknown length
            *     25701  26300: contig of 600 bp in length
            *     26301  26380: gap of unknown length
            *     26381  27488: contig of 1108 bp in length
            *     27489  27568: gap of unknown length
            *     27569  28215: contig of 647 bp in length
            *     28216  28295: gap of unknown length
            *     28296  29440: contig of 1145 bp in length
            *     29441  29520: gap of unknown length
            *     29521  30587: contig of 1067 bp in length
            *     30588  30667: gap of unknown length
            *     30668  32042: contig of 1375 bp in length
            *     32043  32122: gap of unknown length
            *     32123  33740: contig of 1618 bp in length
            *     33741  33820: gap of unknown length
            *     33821  35375: contig of 1555 bp in length
            *     35376  35455: gap of unknown length
            *     35456  36258: contig of 803 bp in length
            *     36259  36338: gap of unknown length
            *     36339  38003: contig of 1665 bp in length
            *     38004  38083: gap of unknown length
            *     38084  39509: contig of 1426 bp in length
            *     39510  39589: gap of unknown length
            *     39590  40719: contig of 1130 bp in length
            *     40720  40799: gap of unknown length
            *     40800  42453: contig of 1654 bp in length
            *     42454  42533: gap of unknown length
            *     42534  43841: contig of 1308 bp in length
            *     43842  43921: gap of unknown length
            *     43922  45410: contig of 1489 bp in length
            *     45411  45490: gap of unknown length
            *     45491  46782: contig of 1292 bp in length
            *     46783  46862: gap of unknown length
            *     46863  48570: contig of 1708 bp in length
            *     48571  48650: gap of unknown length
            *     48651  51042: contig of 2392 bp in length
            *     51043  51122: gap of unknown length
            *     51123  52760: contig of 1638 bp in length
            *     52761  52840: gap of unknown length
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Db 113610  CCCGAGATTAATGTGATCACTGTTAACGTTTTCCGTGAGGTGGACAAGAAGAGAAGAGGGG 113669

Qy    676  gacaaggcaggctacgtggctgttgactgttccagtggccaccctggctgggccgccac   735
                |||||              ||||| ||  ||  |||  |||      ||
Db 113670  GACAAATACCAATTTGTGGATCGGTGAAGATACCCGTGCACGATGTCACCTCCAGATTG   113729

Qy    736  ttcacagacagtggtaccccgtgaccctgccaacaggaagtgggggctctggggtatg    795
                 ||  |||  ||||||| |||  ||
Db 113730  CCCTGGGAACAATGGTATCCCATA------------------CTGAGCGACAAGGCGGGC 113771

Qy    796  ggctcggggggaggaggggggtcagggggcggctcaggggcaaaggagggaggggctgt   855
                 ||| || ||  |  ||       |||
Db 113772  GACAGTCTGGGCAGGACATCGGGCGGCGGCGGCGGCAGTGGGTCCAAGGACAAGGAGCAATTG 113831

Qy    856  cctgctgtcggctgaaggcccgttaccagacaatgagtatcctgccatggagctatat    915
                || | |  |||||  ||  |||||||||||       |||||||
Db 113832  CCCACGCTGAGGATCAAGTGTCGTTCCAGAGCACCACCATCTGCCCATCAATGTGTAC   113891

Qy    916  aaggagtttgcagaatatgtgaccaactaccgcatgctgctgtccgtgctggagccc    975
                 ||||   |||| ||
Db 113892  GGCAACTTTTGACGTACCTCAAGGAGAACTATAAGCCGCGTGTGCGAGACCCTGGAGCCG 113951

Qy    976  gccctcaatgtcaaggcaaggaggtcgtagtgcactggttcacatcctgcaaagc   1035
                 ||           |||||||||||||    ||  |||
Db 113952  GTGATCGGAGTCAAGGCCAAGGAGGACATTGGACAGGCACTGGTGCTGCTGATGCACGCA 114011

Qy   1036  acaggcaaggccaaggactccatatcgccgagaacacgctcgccactaaagccatgtcatg 1095
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Db 114012  CAGGGATTGGCGGCGCCTTCTCCACCGATGTGTGGCCCTGCCCTGCTGCTGCCAGTTGGC  114071

Qy   1096  gagcgggaacacctcatattccgcgagaacacgctcgcccactaaagccatagaagagtat 1155
                | |  |   ||||  | ||| |||   ||  || ||  | |
Db 114072  GATCAGAGG---CTTACCTTCAGGGCCAACTCCTTGGCCACCAAGAGCATGGAGGCATTC 114128

Qy   1156  atgagactgattggccagaaatacctcaaggatgccattgggagttcatccgggctctg   1215
                 ||   ||||  | |||||  |   |    || ||  ||||
Db 114129  CTCAAGCTGACGGCGGCGGCGACAGTATCTGCGAGCAGCACTATCCGCCAATAAACGAGCTA 114188

Qy   1216  tatgaatctgaggagagaactgtgaagtagacccatccaagtgca------cagcgtcc   1266
                 ||   ||  | | |||||   |   | |||        |||   ||
Db 114189  ATTCAGTCGGAGAGGACTGCGAGGTGGATCCCACCACCACGAGCGGGTTCGTCGGCGGGT 114248

Qy   1267  agtctgcagagacgcaccaggccaacctgcggatgtgctgagttggcctgtgcaaggtg   1326
                |   |||  |  |  |||||||||||||
Db 114249  TCGCTGGCAGCGACCAGCACAGGCCGCCGCCTTGCGTGGCCGTCCGAGGGGCTGCCAGTGCATC  114308

Qy   1327  gtcaactcccattgcgtgttcccgaggggagctgaaggaggtgtttgcatcatggcggctg 1386
                || |   ||||||||||||||||||
Db 114309  TTCGAATCGCACAAGCATTTTCCCGCCAGTTACGAAATTGCTTTGCGACGTTCGGGGAG   114368

Qy   1387  cgctgtgcagagcgggggggcgcggaggacattgctgacaggctgatcagcgcctcgctcctc  1446
                 |||||              |||||||  ||||||||||  | |  ||  |
Db 114369  CGCTTGCAGCAGCTGGGCGCCGTCAGGAGATATGGCCGACAACCTGATCTCCGCGAGCATTTTC 114428

Qy   1447  ctgcgcttcctctgcgccgccatcatgtcgcccagtctgttggactgatgcaggagtac   1506
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Db 114429  CTGCGCTTCCTGTGCCCGGCCATCCTGTCCGCCTCGCTCTTCAATATCACCAGCGAACTG 114488

Qy   1507  ccagatgagcagacctcacgacccctcaccctcatcgccaagttatccagaacctgg    1566
                |  | ||||  |||  |||  ||  | || ||
Db 114489  CCGTCCGCACGGCCACCGCCAATCTCACACTGGTGCCAAGACCCTGCAAACATTGGCC  114548

Qy   1567  aacttttccaagttacctcaaagggagactcctgggcttcatgaacgagtttctggag   1626
                 | ||  |||||||||||||||||||||||||
Db 114549  AATTCACCCGCTTCCAGGCAAAGAGAACTTTATGGAGTTTCTCAACGATTTCCTCGAG   114608

Qy   1627  ctggaatggggttctatcgacaattcttgtatgagatatccaacctggacacactgac-  1685
                 |||     | || | || |  |||||||||||||||||
Db 114609  CAGGAGGCCGGCTTCGCATGCAAACTTTGGGGGCTACATAGACTTGGGCCGGAGCTCCCACCCA 114668

Qy   1686  -------caacgagcagcagtttgagggctacatagacttgggccgcgggagctcttccaca 1737
                       ||||||||||||  |||   | |||||||||||| | |||| |
Db 114669  GCTCCAGACTCGATCCTCGATTGGGCCCGGTACATCGACCAGGGCAAACAGTTGTCCATA  114728
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Db 113610 ... (continued sequence contig listing)

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*   54793   56521:  contig of 1729 bp in length
*   56522   56601:  gap of unknown length
*   56602   58938:  contig of 2337 bp in length
*   58939   59018:  gap of unknown length
*   59019   60837:  contig of 1819 bp in length
*   60838   60917:  gap of unknown length
*   60918   62988:  contig of 2071 bp in length
*   62989   63068:  gap of unknown length
*   63069   65583:  contig of 2515 bp in length
*   65584   65663:  gap of unknown length
*   65664   68774:  contig of 3111 bp in length
*   68775   68854:  gap of unknown length
*   68855   71235:  contig of 2381 bp in length
*   71236   71315:  gap of unknown length
*   71316   74113:  contig of 2798 bp in length
*   74114   74193:  gap of unknown length
*   74194   77405:  contig of 3212 bp in length
*   77406   77485:  gap of unknown length
*   77486   80936:  contig of 3451 bp in length
*   80937   81016:  gap of unknown length
*   81017   83357:  contig of 2341 bp in length
*   83358   83437:  gap of unknown length
*   83438   87456:  contig of 4019 bp in length
*   87457   87536:  gap of unknown length
*   87537   91532:  contig of 3996 bp in length
*   91533   91612:  gap of unknown length
*   91613   97143:  contig of 5531 bp in length
*   97144   97223:  gap of unknown length
*   97224  105593:  contig of 8370 bp in length
*  105594  105673:  gap of unknown length
*  105674  112071:  contig of 6398 bp in length
*  112072  112151:  gap of unknown length
*  112152  121011:  contig of 8860 bp in length
*  121012  121091:  gap of unknown length
*  121092  143113:  contig of 22022 bp in length
*  143114  143193:  gap of unknown length
*  143194  143587:  contig of 394 bp in length
*  143588  143667:  gap of unknown length
*  143668  143927:  contig of 260 bp in length
*  143928  144007:  gap of unknown length
*  144008  144842:  contig of 835 bp in length
*  144843  144922:  gap of unknown length
*  144923  145360:  contig of 438 bp in length
*  145361  145440:  gap of unknown length
*  145441  145915:  contig of 475 bp in length
*  145916  145995:  gap of unknown length
*  145996  146532:  contig of 537 bp in length
*  146533  146612:  gap of unknown length
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Query Match   6.0%;   Score 240.2; DB 36; Length 191504;
Best Local Similarity   50.6%;   Pred. No. 8.4e-37;
Matches   748: Conservative   0; Mismatches   683; Indels   48; Gaps   5;

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Qy    376  gaaaggacaaatgagaattgagaatctacagagggctgtgaaacccaacaaggacaacagc  435
                || ||||      |||  | ||| ||   |   | ||  | || |
Db 113379  GAGCGCGACCTTTGGATCTACTCGCCGCAAGTCGATGGATCTGCGAGAGCCACACG  113438

Qy    436  cgccgggtagataacgtgctgaaactatggatcatagagagctggagaagctgcccccag    495
                |  |||||||| ||||||||  |||||| | | |||  |
Db 113439  CGTCGCACGGACAACTCGCTGAAGATGTGGGTGTACGAGGCGAAAAATCGCCGCCCAAG  113498

Qy    496  aagcgatattactgcgagttatgcctggacgacatgctctatgcacggacacttccaag    555
                 |||  |  |  |  ||||||| |||| | |  ||   |   |||||||
Db 113499  AAGCGTTACTTTTGCGAACTGCAATTGGACAACGCGCTCTACGGCCGACTTCCGTGAAG  113558

Qy    556  cccgctcagctcagagacacgtcttttggggcggcagcacttgagtttaacaacctg     615
                |||||||||||||||||||||  |  || ||  | ||  || ||||
Db 113559  CTGCGAGAC-------GGATCTCGTGTTTGGGGGAGCACTTCGATTTCCCCGACATA  113609

Qy    616  cctgctgtccgggcgctcgggctgcatctgacctgactcggacaaaaagcggaagaag     675
                || |  ||  || |||  ||||||||| |  |||      |||| ||| ||||| |
Db 113559  AAGCGTTACTTTTGCGAACTGCAATTGCAATCTAGACTGG... 113609
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Qy   1738 cttcacgccctgctctgggaggtgtgcccagctcagcaaggaagccctcgaagctg 1797
          ||||| |||  |||||| |   ||||| |||| ||| || |     | ||||||
Db 114729 CTACACAGTTGCTCAGCGAAAGCCTGGCCAAGCTGCCGGAGGCCAGCTGCCACGAGCTG 114788

Qy   1798 ggcccgctgccccggctcctcagcgacatcagcacagcc 1836
          | ||| ||||   |||| ||  |||  | |||| |||||
Db 114789 GATCCGTTGCAGCATATTCTCGATGAAATCAGCCGAGCC 114827
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RESULT 14
AC012161/c
LOCUS   AC012161   202741 bp   DNA   HTG   16-NOV-1999
DEFINITION Drosophila melanogaster chromosome X clone BACR01I22 (D1114)
            RPCI-98 01.I.22 map 16B-16D strain y; cn bw sp, *** SEQUENCING IN
            PROGRESS ***, 142 unordered pieces.
ACCESSION   AC012161
VERSION   AC012161.7 GI:6435885
KEYWORDS   HTG; HTGS_PHASE1.
SOURCE   fruit fly.
  ORGANISM Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1 (bases 1 to 202741)
  AUTHORS   Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,
            Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L.,
            Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
            Hinkle,A., Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K.,
            Kearney,L., Lee,B., Lewis,S., Li,P., Ling,H., Moshrefi,A.R.,
            Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S., Pfeiffer,B.,
            Richards,S., Sethi,H., Svirskas,R.R., Wan,K.H., Webster,D.,
            Wooley,P., Yang,S., Yee,M., Yu,C. and Rubin,G.M.
  TITLE   Sequencing of Drosophila melanogaster
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 202741)
  AUTHORS   Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,
            Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L.,
            Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
            Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L.,
            Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P.,
            Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S.,
            Pfeiffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E.,
            Svirskas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and
            Rubin,G.M.
  TITLE   Direct Submission
  JOURNAL   Submitted (21-OCT-1999) Drosophila Genome Center, Lawrence Berkeley
            Laboratory, MS 64-121, Berkeley, CA 94720, USA
COMMENT   On Nov 16, 1999 this sequence version replaced gi:6425635.
            For further information about this sequence, including its location
            and relationship to other sequences, please visit our sequence
            archive web site (http://www.fruitfly.org/sequence/) or send email
            to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet
            the following cutoffs: length >= 200 bases.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 142 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
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REFERENCE   1  (bases 1 to 300994)
  AUTHORS   Adams,M.D., Celniker,S.E., Holt,R.A., Evans,C.A., Gocayne,J.D.,
            Amanatides,P.G., Scherer,S.E., Li,P.W., Hoskins,R.A., Galle,R.F.,
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            Weinstock,G.M., Weissenbach,J., Williams,S.M., Woodage,T.,
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            Gibbs,R.A., Myers,E.W., Rubin,G.M. and Venter,J.C.
  TITLE     The genome sequence of Drosophila melanogaster
  JOURNAL   Science 287 (5461), 2185-2195 (2000)
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REFERENCE   2  (bases 1 to 300994)
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  JOURNAL   Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive,
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us-09-294-298-5.rge

Fri Jan 19 06:20:01 2001

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Job time: 22547 sec

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OM nucleic - nucleic search, using sw model

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Scoring table:  IDENTITY_NUC
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Searched:       280836 seqs, 80580151 residues

Total number of hits satisfying chosen parameters:     561672

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
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SUMMARIES

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c 2	63.4	1.6	7218	1	US-08-232-463-14	Sequence 14, Appl
3	62	1.6	3117	3	US-08-909-954-3	Sequence 3, Appli
4	61	1.5	2580	3	US-09-050-863-2	Sequence 3, Appli
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ALIGNMENTS

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; Sequence 1, Application US/08909954A
; Patent No. 6100058
; GENERAL INFORMATION:
; APPLICANT: Allen, Maxine J.
; APPLICANT: Buckler, Alan J.
; TITLE OF INVENTION: GAP12 Genes and their Uses
; FILE REFERENCE: SEQ-11P
; CURRENT APPLICATION NUMBER: US/08/909,954A
; CURRENT FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3148
; TYPE: DNA
; ORGANISM: H. sapiens
US-08-909-954-1

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Best Local Similarity  50.0%;  Pred. No. 4.8e-06;
Matches 159;  Conservative  0;  Mismatches 159;  Indels  0;  Gaps  0;

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RESULT 2
US-08-232-463-14/c
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Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
;   APPLICANT: DORNER, F.
;   APPLICANT: SCHEIFLINGER, F.
;   APPLICANT: FALKNER, F. G.
;   TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
;   NUMBER OF SEQUENCES: 52
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Foley & Lardner
;     STREET: 1800 Diagonal Road, Suite 500
;     CITY: Alexandria
;     STATE: VA
;     COUNTRY: USA
;     ZIP: 22313-0299
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/232,463
;     FILING DATE:
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US/07/935,313
;     FILING DATE:
;     APPLICATION NUMBER: EP 91 114 300.6
;     FILING DATE: 26-AUG-1991
;   ATTORNEY/AGENT INFORMATION:
;     NAME: BENT, Stephen A.
;     REGISTRATION NUMBER: 29,768
;     REFERENCE/DOCKET NUMBER: 30472/114 IMMU
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (703)836-9300
;     TELEFAX: (703)683-4109
;     TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 7218 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   IMMEDIATE SOURCE:
;     CLONE: pTZgpt-F1s
US-08-232-463-14

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Db  1256  RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1197

Qy  3404  gcttgaggcagcagcaggtggagaaggactcccagatcaagagcatcattggcaggctga 3463
          :::|::::|::|:| :::::::::::::::::::::::::::::::::::: ::: :: :
Db  1196  RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1137

Qy  3464  tgctggtggaggaggagctgcgccggacaccccgccaccccgaacctgagccgctgccgaac 3523
```

```
Db  1136  RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1077

Qy  3524  ccaagaagaggctgctcgacgctcagagagaggagc 3558
          :::::: ||  ||  ||||
Db  1076  RRRRRRRRRRATCGCAAGCTCCCTGACCTGCAGC 1042

RESULT  3
US-08-909-954-3
; Sequence 3, Application US/08909954A
; Patent No. 6100058
; GENERAL INFORMATION:
;   APPLICANT: Allen, Maxine J.
;   APPLICANT: Buckler, Alan J.
;   TITLE OF INVENTION: GAP12 Genes and their Uses
;   FILE REFERENCE: SEQ-11P
;   CURRENT APPLICATION NUMBER: US/08/909,954A
;   CURRENT FILING DATE: 1997-08-12
;   NUMBER OF SEQ ID NOS: 15
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 3117
;   TYPE: DNA
;   ORGANISM: M. musculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (0)...(0)
US-08-909-954-3

Query Match           1.6%;   Score 62;   DB 3;   Length 3117;
Best Local Similarity  49.7%;  Pred. No. 1.1e-05;
Matches 158;  Conservative  0;  Mismatches 160;  Indels  0;  Gaps  0;

Qy  1261  gcgtccagtgtgcagagcaccaggccaacctgccggatgtgctgtgagattggccctgtgc 1320
          ||||| :|| || || |||| ||  ||   |  | |  |||  |||  || |
Db  1347  gagaccagccgctgggcgtgctgaccggatacctaggtccgttggacgccatcgtgagc 1406
Qy  1321  aaggtgtcaactcccattgcgtgttcccgagggagctgaaggaggtgtttgtcatcatgg 1380
          || ||| | |||  :| |  ||  |:|| |:|| :| ||  :||  | | |
Db  1407  tctacaggggctgcccacttgccttgccttaagcagctccagcggtgtgtg 1466
Qy  1381  cggctgccgtgtcgacagcggggcgcggggaggacattgctgacaggctgatcagccgcctcg 1440
          |||| | ||| ||| |||| ||  ||  || |||| ||| |||| |||| |
Db  1467  gagaagcgcttctctgggatagagcatcaggatgtgaagtacctggccatcagtggcttc 1526
Qy  1441  ctcttcctgcgcttcctcgccgcgcatcatcgtcgccagtcgttggactgatgcag 1500
          ||||| ||| |||| || || ||||| | |   |||| |  ||||| |||  ||  |
Db  1527  ctcttctgcggttctttgcgctgcatcctcacaccgaaacctgttgacctcagagac 1586
Qy  1501  gagtaccagatgagcagacctcacgaacctcagccaagttatccgaac 1560
          ||  || ||  | |  |||| | || ||  |||| |||||   || ||
Db  1587  cagcacgcagaccccccagaccagccgttccctgctgctctcgccaaggctgtcagagc 1646
Qy  1561  ctggccaactttccaag 1578
          ||| |||| |||| |||
Db  1647  attgggaacctgggccag 1664

RESULT  4
US-09-050-863-2
; Sequence 2, Application US/09050863
; Patent No. 611411l
; GENERAL INFORMATION:
;   APPLICANT: Lao, Ying
;   APPLICANT: Hiang, Betty
;   APPLICANT: Payan, Don
;   TITLE OF INVENTION: Mammalian Protein Interaction Cloning
;   TITLE OF INVENTION: System
;   NUMBER OF SEQUENCES: 5
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
```

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               GenCore version 4.5
        Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:      January 18, 2001, 20:02:07 ; Search time 505.11 Seconds
                                           (without alignments)
                                           2960.767 Million cell updates/sec

Title:             US-09-294-298-5
Perfect score:     3981
Sequence:          1 taggagagactgagctgcc........tggggtgctatcccatcct 3981

Scoring table:     IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched:          480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters:       960044

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing:   Minimum Match 0%
                   Maximum Match 100%
                   Listing first 45 summaries

Database :   N_Geneseq_36:*
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    6:  /SIDS6/gcgdata/geneseq/geneseqn/NA1985.DAT: *
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   19:  /SIDS6/gcgdata/geneseq/geneseqn/NA1998.DAT: *
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   21:  /SIDS6/gcgdata/geneseq/geneseqn/NA2000.DAT: *
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Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	95.8	2.4	2647	18	T76739	cDNA encoding acti
2	63.6	1.6	1337	20	Z17263	Human gene express
3	61	1.5	795	19	V55830	FLGA insert stabil
4	61	1.5	799	19	V55831	Nucleotide sequenc
5	61	1.5	5452	20	X90923	Anti-sense strand
c 6	61	1.5	8705	20	Z23778	Vector pShuttle DN
c 7	61	1.5	9600	19	V21683	Vector plasmid pCM
8	61	1.5	10380	20	Z22248	Nucleotide sequenc
9	61	1.5	10596	14	Q51731	Plasmid pCIsEBON f
10	61	1.5	10596	17	T40348	Plasmid pCIsEBON f
11	61	1.5	10596	20	X15650	Nucleotide sequenc
12	59.6	1.5	1925	20	X90924	Epstein Barr Virus
c 13	59.4	1.5	1908	8	N71064	Gene encoding Plas
14	59.2	1.5	1000	21	A02484	Human colon cancer
c 15	57.8	1.5	49999	20	Z23895	Murine LOBO homolo
16	57.6	1.4	2338	19	V23249	Nephila clavipes s
17	57.6	1.4	2338	21	Z38195	N. clavipes spider
18	56	1.4	2000	8	N71065	Gene encoding Plas
19	56	1.4	2338	12	Q14183	N.clavipes draglin
c 20	56	1.4	16442	18	X83006	Partial mouse WRN
21	55.8	1.4	2004	18	T85356	Nephila clavipes s
c 22	54.6	1.4	32207	20	V73805	KSHV LUR DNA (nucl
c 23	54.6	1.4	137507	19	V19941	KSHV long unique c
24	54.4	1.4	9551	20	Z22301	cDNA encoding a hu
25	54	1.4	543	13	Q23092	Antigen tc-7a gene
26	53.6	1.3	1995	12	Q14184	N.clavipes draglin
27	53.6	1.3	1995	19	Z38196	Nephila clavipes s
28	53.6	1.3	1995	21	Z38196	N. clavipes spider
29	53.4	1.3	4055	20	Z40484	Human ZC2 DNA. Ho
30	53.4	1.3	4180	21	A10669	Human protein kina
31	53	1.3	1137	14	Q33061	Plasmodium vivax c
c 32	52.4	1.3	114955	19	X53491	Human adenosine Al
33	52.2	1.3	1847	19	V04694	Cell cycle protein
34	51.4	1.3	3198	20	X02974	Human IL-1ra BAC c
35	51.2	1.3	2744	16	Q98470	MiSP1-containing p
c 36	51.2	1.3	51259	18	X83007	Partial mouse WRN
c 37	51	1.3	10732	21	A10594	Gene encoding a su
38	50.2	1.3	1686	16	Q87587	DNA encoding Leuco
39	49	1.2	2040	18	T62137	Leishmania brazil
40	49	1.2	2040	19	V47557	Leishmania antigen
c 41	48.8	1.2	1218	21	A02488	Human colon cancer
42	48.8	1.2	2313	20	Z07197	Human lung tumour
43	48.6	1.2	1432	19	V47585	Leishmania antigen
44	47.8	1.2	3337	17	T34620	P. vivax ESP-1 blo
45	47.8	1.2	3337	20	X15174	DNA encoding a sec

ALIGNMENTS

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RESULT     1
T76739
ID   T76739 standard; cDNA; 2647 BP.
XX
AC   T76739;
XX
DT   08-OCT-1997  (first entry)
XX
DE   cDNA encoding active type R-Ras protein binding protein p98.
XX
KW   Active-type-R-Ras protein; p98; tumour; disease; cancer;
KW   cellular Ca ion; phospholipid; tumour forming promoter;
KW   tumour forming inhibitor; ss.
XX
OS   Bos taurus.
XX
FH   Key             Location/Qualifiers
FT   CDS             13..2517
FT                   /*tag= a
FT                   /product= p98
XX
PN   JP09135688-A.
XX
PD   27-MAY-1997.
XX
PF   16-NOV-1995;   953P-0298720.
XX
PR   16-NOV-1995;   953P-0298720.
XX
PA   (KIRI ) KIRIN BREWERY KK.
XX
DR   WPI; 1997-335993/31.
DR   P-PSDB; W24227.
XX
PT   Active R-Ras protein-binding protein p98 - used in the treatment of
```

```
PT   cancer, and diseases related to cellular calcium ion concentrations
XX
PS   Claim 9; Page 9-12; 18pp; Japanese.
XX
CC   This sequence encodes a protein capable of binding to active-type-R-Ras
CC   protein.  The protein has a molecular weight of 98 kD by SDS-PAGE, and
CC   is designated p98.  The protein coding sequence can be inserted into a
CC   suitable vector to treat certain tumours or diseases (various cancers)
CC   in which active R-Ras protein in involved.  Because active R-Ras protein
CC   is involved in formation and inhibition of tumours and related to
CC   diseases in which cellular Ca ions or phospholipids are involved, the
CC   screening method can be used for screening e.g. a tumour forming promoter
CC   or tumour forming inhibitor.
XX
SQ   Sequence 2647 BP; 633 A; 764 C; 769 G; 481 T; 0 other;

Query Match              2.4%;     Score 95.8;  DB 18;  Length 2647;
Best Local Similarity   50.9%;     Pred. No. 1.5e-12;
Matches  310;  Conservative    0;  Mismatches  287;   Indels   12;  Gaps    3;

Qy    987 caaggcaaggaggagtcgtagtgcactggttcacatcctgcaaagcaagcaagc 1046
           || || ||| ||||| |||||| || ||  | |||| | |||| ||| |||| |||
Db    996 caggagaagcaggaggcggccatcccgtcggtgcggcttcctgcattacggccgggt 1055

Qy   1047 caaggacttccttcagacatggccatgtcagaggtagaccggttcatggacgcgggaaca 1106
           | |||||| ||||| |||| ||| |||| | |||| |  | |  |||| |  |||| || 
Db   1056 ggtgccctcatcagcgctcatcgcagcgccgaggtccgcaggacccaggacc--ccaa 1112

Qy   1107 cctcatattccgcgagaaacacgctcgccactaaagccatagaaagatatagagacttgat 1166
           || |||||| |||| |||| |||| |  | ||||||| | ||||  |||| |||
Db   1113 tacgtatcttccgagggaactgctgacatccaagtgcatcgagacgataagcggc 1172

Qy   1167 tggccagaaataccctcaaggatgccattgggagttcatccgggctctgtgatctga 1226
           || | ||||| ||  |||| |||| ||||| ||| ||||| ||| |||||
Db   1173 aggcatgcagtacctacacgtcaccctgaaaccaccatagaggagattgccagagtca 1232

Qy   1227 ggagaactgaagtagaccccatcaagtgcacacgtcc---agtctgcagagcacca 1283
           || ||||| || |||||||||| |||||  || | |     |||| || ||  ||
Db   1233 taagtcctgtgaaattgacccgtgaggctgaaggacggcgagagccctagagagcaacat 1292

Qy   1284 ggccaactgcggatgtgctgtgacccatcaagtggtcaactccattgcgt 1343
           ||  |||||||| ||| || ||  | ||| | |  ||  ||| | ||
Db   1293 gggagaacctgcggcagtttgtggaccgcgttcagcgtcatcaccaaatcggggggtgag 1352

Qy   1344 gttcccgaggagctgaagaggtgtttgcatcatcggccggctgctgtgcagacgggg 1403
           ||||  |||||| ||  |  | ||| ||  |  |||||| ||||| || |||
Db   1353 ctgccccaccgtcatgtgtgacatcttctctcccgcggaggcagccgccaagcgctt 1412

Qy   1404 ccgggaggacattgctg------acaggctgatcagcgcctcgctcttcctgcgcttcct 1457
           || |||| ||| | ||        |||| || |  ||||||||| ||||| |||
Db   1413 ccaggatgacctggacgtgcggtacacagcgtgagcagcttcattttctcgggttctt 1472

Qy   1458 ctgccggccatcatgtcgcccagtctgtttggactgtgcaggagtaccagatgagca 1517
           | | ||||||| | ||  | ||||| ||  |  || || || |
Db   1473 cgctccagccatcctgtccccaaccttccagctcacgcccaccacacggaccccaca 1532

Qy   1518 gacctcacgaacctcaccctcatcgccaagttatccagaacctggccaactttccaa 1577
           ||| |||| | |||| |||||| ||| |  |  ||| ||  |||| ||||| |||
Db   1533 gacgtcgaggacgctgacacttgttcgaagacaccattcagactctggcagcctgtccaa 1592

Qy   1578 gtttacctc 1586
           || | ||
Db   1593 gtccaagtc 1601


RESULT  2
Z17263
ID   Z17263 standard; cDNA; 1337 BP.
XX
AC   • Z17263;
XX
DT   12-OCT-1999  (first entry)
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XX
DE   Human gene expression product cDNA sequence SEQ ID NO:4735.
XX
KW   Human; gene; gene expression product; diagnosis; therapy; probe;
KW   detection; mapping; tissue typing; profiling; forensic; cancer;
KW   genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9938972-A2.
XX
PD   05-AUG-1999.
XX
PF   28-JAN-1999;      99WO-US01619.
XX
PR   03-APR-1998;      98US-0080666.
PR   28-JAN-1998;      98US-0072910.
PR   24-FEB-1998;      98US-0075954.
PR   31-MAR-1998;      98US-0080114.
PR   03-APR-1998;      98US-0080515.
XX
PA   (CHIR ) CHIRON CORP.
PA   (HYSE-) HYSEQ INC.
XX
PI   Crkvenjakov R, Dickson M, Drmanac R, Drmanac S;
PI   Escobedo J, Garcia PD, Garcia V, Giese K, Innis MA;
PI   Jones WL, Kassam A, Kennedy GC, Kita D, Labat I;
PI   Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinhard C;
PI   Stache-Crain B, Sudduth-Klinger J, Williams LT;
XX
DR   WPI; 1999-49092/41.
XX
PT   Novel human genes and their expression products which are
PT   differentially expressed in different cell types
XX
PS   Claim 1; Page 2250-2251; 2479pp; English.
XX
CC   The present invention describes a library of human polynucleotides
CC   comprising the sequences given in Z12532 to Z17779. Also described is a
CC   method of detecting differentially expressed genes correlated with the
CC   cancerous state of a mammalian cell, comprising detecting at least one
CC   differentially expressed gene product in a test sample from a cell
CC   suspected of being cancerous, where the gene product is encoded by one
CC   of the 5248 polynucleotide sequences given in Z12532 to Z17779. The
CC   polynucleotides can be used as a source of primers and probes, which can
CC   be used for a variety of purpose, e.g. detection of expression levels,
CC   mapping, tissue typing or profiling, forensics, genetic analysis and
CC   detection of polymorphisms. Polypeptides encoded by the polynucleotides
CC   can be used for raising antibodies for experimental, diagnostic and
CC   therapeutic purposes. The polynucleotides may also be used to construct
CC   arrays for diagnostics (which may be used to determine function of an
CC   encoded protein); and to detect differences in expression levels between
CC   two cells (e.g. to identify abnormal or diseased tissue in a human, to
CC   identify a genetic predisposition or susceptibility to a disease such as
CC   cancer). The polynucleotides of the invention are especially used in the
CC   diagnosis, prognosis and management of colorectal cancer, breast cancer,
CC   and lung cancer. The polynucleotides can also be used to screen for
CC   peptide analogues and antagonists.
XX
SQ   Sequence 1337 BP; 42 A; 577 C; 27 G; 22 T; 669 other;

Query Match              1.6%;     Score 63.6;  DB 20;  Length 1337;
Best Local Similarity   33.0%;     Pred. No. 2.5e-05;
Matches  147;  Conservative    0;  Mismatches  298;   Indels    0;  Gaps    0;

Qy   3535 ctgctcgacgctcagagaggcagcttccccccttgggtccaacaaccgcgtgacgc 3594
           | ||||  |||||| ||| ||| |||  | ||||||
Db    419 cnncncccnnncnccnnnnnncnccccncnnnnnncnnnnccccccnnnnnnc 478

Qy   3595 tggcccacttggaacggcctggcccccccagcccaccccccccccgccggctcgaga 3654
           ||| ||| |||||  |||| ||||||  || | |||||| |||| ||| ||||
Db    479 nncccccnncncncccccccnnnnnnnnnnnnnnnnnnnnnnnccnnnnnnnnc 538
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 18, 2001, 07:58:49 ; Search time 6516.34 Seconds
                                             (without alignments)
                                             4281.055 Million cell updates/sec

Title: US-09-294-298-5
Perfect score: 3981
Sequence: 1 taggagagactgagctgcc.........tgggtgctatcccatcct 3981

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 7991742 seqs, 3503743858 residues

Total number of hits satisfying chosen parameters: 15983484

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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145:  gb_est85:*
146:  gb_est86:*
147:  gb_est87:*
148:  gb_gss1:*
149:  gb_gss2:*
150:  gb_gss3:*
151:  gb_gss4:*
152:  em_gss1:*
153:  em_gss2:*
154:  em_gss3:*
155:  em_gss4:*
156:  gb_gss5:*
157:  gb_gss6:*
158:  gb_gss7:*
159:  gb_gss8:*
160:  gb_gss9:*
161:  em_gss5:*
162:  em_gss6:*
163:  em_gss7:*
164:  em_gss8:*
165:  em_gss9:*
166:  gb_gss10:*
167:  gb_gss11:*
168:  gb_gss10:*
169:  gb_gss11:*
170:  em_gss12:*
171:  gb_gss12:*
172:  gb_gss13:*
173:  gb_gss14:*
174:  gb_gss15:*
175:  gb_gss16:*
176:  gb_gss17:*
177:  gb_gss18:*
178:  gb_gss19:*
179:  em_gss13:*
180:  gb_gss20:*
181:  gb_gss21:*
182:  gb_gss22:*
183:  gb_gss23:*
184:  gb_gss24:*
185:  em_gss14:*
186:  em_gss15:*
187:  em_gss16:*
188:  em_gss17:*
189:  em_gss18:*

190:  gb_gss25:*
191:  gb_gss26:*
192:  gb_gss27:*
193:  gb_gss28:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		490.4	12.3	571	37	AV590698	AV590698 AV590698
2		383.8	9.6	474	181	AZ399131	AZ399131 1M0164P14
3		294.6	7.4	593	95	AW779747	AW779747 hn85f10.x
4	c	250.4	6.3	463	108	BE463433	BE463433 hw23d06.x
5	c	244.6	6.1	427	11	AA709010	AA709010 zf94h11.s
6	c	233.6	5.9	597	90	AW421227	AW421227 fj94f10.x
7		228.8	5.7	682	173	AQ993964	AQ993964 RPCI-23-2
8		222	5.6	566	22	AI606711	AI606711 ml58d01.Y
9		220.2	5.5	413	10	AA691827	AA691827 vt05d01.r
10		214	5.4	707	28	AJ396547	AJ396547 AJ396547
11		210.2	5.3	555	27	AI958829	AI958829 fd22g01.y
12	c	201	5.0	628	108	BE490923	BE490923 db38g08.x
13	c	197.2	5.0	516	111	BE695645	BE695645 MR1-BT080
14	c	195.8	4.9	347	87	AW204612	AW204612 UI-H-BI1-
15	c	195.4	4.9	596	136	BE848541	BE848541 uw39f05.y
16	c	190	4.8	481	135	BE773015	BE773015 RC1-FT013
17		185	4.6	542	93	AW556799	AW556799 109245 MA
18		180.6	4.6	296	23	AI650331	AI650331 wa18f01.x
19		177.6	4.5	345	39	AW076911	AW076911 fj03d08.y
20		173	4.3	511	22	AI577567	AI577567 UI-R-Y0-v
21		168.8	4.2	388	183	B68206	B68206 CIT978SK-A-
22	c	165.6	4.2	474	87	AW205989	AW205989 UI-H-BI1-
23	c	161.2	4.0	460	22	AI609604	AI609604 tw91e09.x
24	c	157	3.9	449	9	AA554056	AA554056 n101g07.s
25		156.2	3.9	1020	191	CNS02VGW	AL215753 Tetraodon
26		154.6	3.9	440	2	AA107246	AA107246 ml58d01.r
27	c	149.4	3.8	651	19	AI327335	AI327335 mp74c11.x
28	c	148.6	3.7	877	192	CNS04DL0	AL285885 Tetraodon
29	c	146.8	3.7	443	40	AW136165	AW136165 UI-H-BI1-
30	c	146.8	3.7	464	95	AW826497	AW826497 fk62h05.x
31		146	3.7	452	9	AA554055	AA554055 n101g06.s
32		145.4	3.7	407	133	BE015978	BE015978 fk62h05.y
33	c	139.8	3.5	382	22	AI562171	AI562171 vw73f04.x
34	c	138.6	3.5	317	91	AW527364	AW527364 UI-R-BO1-
35		138.6	3.5	457	2	AA118397	AA118397 mp74c11.r
36	c	138.4	3.5	268	92	AW593427	AW593427 hg15e10.x
37	c	136.6	3.4	379	9	AA575948	AA575948 um56e05.s
38		135.6	3.4	554	111	BE723198	BE723198 192621 MA
39	c	133.4	3.4	336	26	AI874961	AI874961 u127f03.x
40		131.8	3.3	694	28	AJ399084	AJ399084 AJ399084
41		130.4	3.3	335	134	BE085114	BE085114 CM2-BT066
42	c	128.4	3.2	1006	190	CNS00HWF	AL073826 Drosophil
43	c	128.2	3.2	631	191	CNS01XQ5	AL172022 Tetraodon
44		125.2	3.1	975	191	CNS03ANH	AL235430 Tetraodon
45	c	124.2	3.1	397	111	BE695651	BE695651 MR1-BT080

ALIGNMENTS

```
RESULT     1
AV590698
LOCUS        AV590698         571 bp    mRNA                          EST       29-AUG-2000
DEFINITION   AV590698 Bos taurus brain fetus Bos taurus cDNA clone E1BR014B04
             5', mRNA sequence.
ACCESSION    AV590698
VERSION      AV590698.1   GI:9701691
KEYWORDS     EST.
SOURCE       cow.
```

Qy 1531 ctcaccctcatcgccaaggt 1551
         ||||| ||||||||||| |
Db   551 CTCACCCTCATCGCCAAGGGT 571

RESULT 2
AZ399131/c
LOCUS   AZ399131   474 bp   DNA   GSS   03-OCT-2000
DEFINITION 1M0164P14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0164P14 R, DNA sequence.
ACCESSION   AZ399131
VERSION   AZ399131.1 GI:10514203
KEYWORDS   GSS.
SOURCE   house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 474)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes.R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
TITLE   Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0164   row: P   column: 14
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 474.
FEATURES   Location/Qualifiers
     source   1..474
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0164P14"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from a
                     musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT   92 a   151 c   131 g   100 t
ORIGIN

Query Match   9.6%;   Score 383.8; DB 181; Length 474;
Best Local Similarity 93.7%;   Pred. No. 3.1e-79;
Matches 400; Conservative   0; Mismatches   27; Indels   0; Gaps   0;

ORGANISM   Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1 (bases 1 to 571)
AUTHORS   Sugimoto,Y., Hirotsune,S., Takasuga.A., Itoh.R., Jitohzono,A. and
            Suzuki,H.
TITLE   bovine cDNA sequencing
JOURNAL   Unpublished (2000)
COMMENT   Contact: Yoshikazu Sugimoto
            Animal Genetics Division
            Shirakawa Institute of Animal Genetics
            Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
            Tel: 81-248-25-5641
            Fax: 81-248-25-5725
            Email: kazusugi@cocoa.ocn.ne.jp
            Single pass sequencing.
            This clone was obtained from a polyA-deleted cDNA library.
FEATURES   Location/Qualifiers
     source   1..571
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
                     /clone="E1BR014B04"
                     /clone_lib="Bos taurus brain fetus"
                     /tissue_type="brain"
                     /dev_stage="fetus"
                     /lab_host="DH10B"
                     /note="Vector: pZL1; Site_1: SalI; Site_2: NotI; Poly A
                     was deleted from a NotI site"   1 others
BASE COUNT   124 a   161 c   169 g   116 t   1;
ORIGIN

Query Match   12.3%;   Score 490.4; DB 37; Length 571;
Best Local Similarity 93.2%;   Pred. No. 3.8e-104;
Matches 523; Conservative   0; Mismatches   37; Indels   1; Gaps   1;

Qy   992 gcaaggaggaggtcgctagtcacactgttcacatcctgcaaagcacaggcaaggccaagg 1051
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   11 GCAAGGAGGAGGTCGCCAGTGCTCTGGTTCACATCCTGCAAGTACAGGCAAGGCCAAGG 70

Qy 1052 acttcctttcagacatggccatgtcagaggtagaccggttcatggagcggaacacctca 1111
         ||||||||||||||||||||||||| ||||||| ||||||| || ||||||| ||||||||
Db   71 ACTTCCTTTCAGACATGGCCATGTCCGAGGTGGACCGGTTCATGGAACGAGAACACCTCA 130

Qy 1112 tattccgagaacacgctcgccactaaagccataagaagagagtatatgagactgattggcc 1171
         ||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db   131 TATTCCCGAGAACACGCTCGCCACTAAAGCCATAGAAGAGTACATGAGACTGATTGGTC 190

Qy 1172 agaaatacctcaaggatgccattgggagttcatccgggctctgtatgaatctgagaga 1231
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   191 AGAAATACCTCAAGGATGCCATCGGGGAATTCATCCGTGCTCGTGCTATGAATCTGAGGAGA 250

Qy 1232 actgtgaagtagacccataagtgcacagcgtccagtctgcgagagcaccaggccaacc 1291
         ||||| || |||||||||||||| | |||| |||| ||||||||||||||||||||||||
Db   251 ACTGTGAGGTGACCCCATCAAGTGCACGGCATCCAGTTTGGCTGAGCACCAGGCCAACC 310

Qy 1292 tgcggatgtgctgtgagttggcctgtcaagtggtcaactccattgcgtgttcccga 1351
         ||||||||| || |||||||||||||||||||||||||||||||||||||||||||||
Db   311 TGCGGATGTGCTGTGAGTTGGCCCTGTCAAGGTGGTCAACTCCCATTGCGTGTTCCCGA 370

Qy 1352 gggagctgaaggaggtgtttgcatcatggcggctgcctgtgcagagcgcggcgggagg 1411
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   371 GGGAGCTGAAGGAGGTGTTTGCCTCCTGCGACTTGCGCGCTGTGCAGAGCGGGGCCGAGAGG 430

Qy 1412 acattgctgacaggctgatcagcgctcgctcctctctcgccggccatca 1471
         ||||||| ||| |||||||||||||||||||||||||||||||||||||| |
Db   431 ACATTGCGGACCGGCTGATCAGCGCCCTCGCTCCTCTCGCCGGCTTCCTCGCTCCTGCCGGCCATTA 490

Qy 1472 tgtcgcccagtcgtt-tggactgatgcagaggagtacccagatagcagacctcacgaacc 1530
         ||||||| ||| || || |||||||||||||||||||||||||||||| || ||||
Db   491 TGTCGCCCAGCCTNTTCGGGGTCATGCAGGAGTACCCAGATGAGCAAACTTCGAGAACC 550

```
                                     Plasmid DNA from the normalized library NCI_CGAP_Kid3 was
                                     prepared, and ss circles were made in vitro. Following HAP
                                     purification, this DNA was used as tracer in a subtractive
                                     hybridization reaction. The driver was PCR-amplified cDNAs
                                     from a pool of 5,000 clones made from the same library
                                     (cloneIDs 1322376-1323911, 1456007-1456775, and
                                     1500552-1502855). Subtraction by Bento Soares and M.
                                     Fatima Bonaldo."

BASE COUNT        104 a        169 c        178 g        141 t        1 others
ORIGIN

Query Match           7.4%;      Score 294.6; DB 95;   Length 593;
Best Local Similarity 73.0%;      Pred. No. 2.3e-58;
Matches  378;  Conservative   0;  Mismatches 140;  Indels   0;  Gaps   0:

Qy  841 gggaaggaggctgcctgctgtggcgctgaagcgcccgttaccagacaatgagtatcctg 900
            || ||||||| | ||||| || | ||||||||||||||| || || | |||||||| ||
Db  518 GGCAAGGGCACTGGACCATGATCAGCATCAGCATCAAGGCGCGCTACCAAACCATCACCATCACCTG 459

Qy  901 cccatggagctatataaggagtttgcagaatatgtgaccaaccactaccgcatgctgtgt 960
            |||||||| | |||| || | ||| || | |||||||||||  | | ||||||||||||
Db  458 CCCATGGAGATGTACAAAGAGTTCGCTGACGACCATCAACCAACCACTACCTGTGCCTGTGT 399

Qy  961 gccgtgctggagcccgccctcaatgtcaagggcaaggaggaggtcgctagtgcactggtt 1020
            || | ||||||||| |||| |||||| | ||| ||||||||| || | ||| |||||
Db  398 GCAGCCCTCGAGCCCATCCTCAGTGCCAAGACCAAGGAGGAGATGGCATCGCCCTGGTG 339

Qy  1021 cacatcctgcaaagacacagcgcaaggccaaggacttcctttcagacatggccatgtcagag 1080
             |||||||||| ||||||| |||| ||||| ||| |||||||||| ||||||||  |||||||
Db  338 CACATCCTGCAGAGCACGGCAAGGTGAAGGACTTCCTGACAGACCTGATGATGTCAGAG 279

Qy  1081 gtagacggttcatggagcggaacacctcatattccgcgagaacacgctcgccactaa 1140
             |||||| | | |||| ||| | |||||||| |||||||| ||| |||||| ||||||||
Db  278 GTGGACCGCTGCGGGAGCACAGAGCACCTCATCTTCCGGGAGAACACACTGGCCACCAAG 219

Qy  1141 gccatagagagtatatgagactgattggccagaaatacctcaaggatgccattgggggag 1200
             |||||| | |||||| |  |  | || || |||||||| |||||| || || || ||||
Db  218 GCCATTGAGGAGTACCTCAAGCTAGTGGGCCAGAAGTACNTGCAGGACGCGCCCTAGGTGAG 159

Qy  1201 ttcatccgggctcgtgtatgatctgaggagaaactgtgaagtagaccccatcaagtgcaca 1260
             ||||| || |||||| | | ||||||  | | |||||| |||| | || ||||| || |||
Db  158 TTCATCAAGCCGTGTATGACTCAGATGAGACAGGAGAACGGCAGGTGATCCCAGACAAGTGCTCG 99

Qy  1261 gcgtccagtcttggcagagcaccaggccaacctgcggatgtgtgagtggccctgtc 1320
             || |  |||||| || ||| ||| |||||||||||||||||||||||| ||||||||
Db   98 GCGCCTGACCTCGACCAGCACCAGGCAACCTCAAGATCTGCTGCGAGCTGGCCTTCTGC 39

Qy  1321 aaggtggtcaactccattgcgtgtcccgagggagct 1358
             |||||||||||| |||||||||| ||||||||| |||||
Db   38 AAGATCATCAACTCCTACTGTCTTCCCACGGGAGTT 1


RESULT   4
BE463433/c
LOCUS       BE463433       463 bp    mRNA                      EST       27-JUL-2000
DEFINITION  hw23d06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3183755 3'
            similar to TR:O95174 O95174 NGAP. ; mRNA sequence.
ACCESSION   BE463433
VERSION     BE463433.1  GI:9509206
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 463)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
  COMMENT   Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
```

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Qy  423 caggacaacagccgccgggtagataacgctgctgaaacatggatcatagaagctcgaga 482
            | |||||||||||||||||||||||||||||| |||||| |||||||||||||||
Db  427 CCAGGACAACAGCCGCCGAGTAGATAAACGTGCTGAAGCTATGGATCATAGAGGCTCGAGA 368

Qy  483 gctgcccccaagagcgatattactgcgagttatgcctggacgacatgctctatgcacg 542
            ||||||||||||||| ||||||||||||||| | ||||||| | |||||||||||
Db  367 GCTGCCCCCCAAGAGCGATATTACTGTGAGCTGTGCCTGGACGACATGCTGTATGCACG 308

Qy  543 gaccacttccaagcccgctcagcctcaggagacactgtctttggggcgagcacttcga 602
            ||||| |||||||||||||| |: |||||||||||||| ||||||||||||||||| ||
Db  307 AACCACCTCCAAGCCCCGCTCGGCTCAGGACGACACCGTCTTTTGGGCCGAGCACTTTGA 248

Qy  603 gttaacaacctgcctgctgtccgggcggctgccggctgcatctgaccgtgactcggacaa 662
            ||||||| || | ||||||||| |||| ||| |||||| |||| |||||||||||||
Db  247 GTTTAACAACCTGCCTGCCGTCCGGCCTGCCGGCCCTTCGGCTGCCATCTGACCGTGACTCAGACAA 188

Qy  663 aaagcggaagaagaaggcaggctacgttggctctgttcagtggcaccct 722
            ||||||||||||||||||| |||||||||||| ||||||||||||||||
Db  187 AAAGCGGAAGAAGAAGGCTGGCTACGTTGGCTCGGTGACTGTGTTCCAGTGGCCACCCT 128

Qy  723 ggctgggcgccacttcacagagcagtggtaccccgtgaccctgccaacagaaagtgggg 782
            ||||||||||||||||||||||||| |||||||| ||| | || ||||||||||||
Db  127 AGCTGGGCGGCCCACTTCACAGAGCAGTGGTACCCCGTGACCTTGCCGACAGGCAGTGTGGGG 68

Qy  783 ctctggggtatgggctcgggggagggggaggggggtcaggggcgctcaggggcaaagg 842
            |||||||| | | |||||||||||||||||||||||| |||| ||||||||||||||||
Db   67 CTCTGGGGCGCATGGGCTCGGGGGAGGAGGGGGGTGGCTCAGGGGCAAAGG 8

Qy  843 gaaagga 849
            |||||||
Db    7 GAAAGGA 1


RESULT   3
AW779747/c
LOCUS       AW779747       593 bp    mRNA                      EST       12-MAY-2000
DEFINITION  hn85f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3034699 3'
            similar to TR:O95174 O95174 NGAP. ; mRNA sequence.
ACCESSION   AW779747
VERSION     AW779747.1  GI:7794350
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 593)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
  COMMENT   Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL, send email to:
            info@image.llnl.gov
            Seq primer: -40UP from Gibco
            High quality sequence stop: 451.
FEATURES             Location/Qualifiers
     source          1..593
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3034699"
                     /clone_lib="NCI_CGAP_Kid11"
                     /lab_host="DH10B"
                     /note=/organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
                      a modified polylinker; Site_1: Not I; Site_2: Eco RI;
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